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OM nucleic - nucleic search, using sw model

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                        GenCore version 5.1.7

Run on:      April  3, 2006, 05:39:11 ; Search time 172 Seconds
                                         (without alignments)
                                         6118.119 Million cell updates/sec

Title:           US-10-624-670-1
Perfect score:   592
Sequence:        1 ctataaggcacgcgtggtcg.........gcccgtcgggaggcgccatg 592
Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters:     2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  Issued Patents NA:*
   1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
   2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
   3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
   4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
   5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
   6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
   7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
   8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
   9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	310	52.4	982	3	US-08-725-532A-4	Sequence 4, Appli
	2	310	52.4	982	3	US-09-016-434-993	Sequence 993, App
	3	234	39.5	1315	3	US-09-164-193-1	Sequence 1, Appli
	4	234	39.5	1315	2	US-09-221-448A-1	Sequence 1, Appli
	5	52.8	8.9	7218	3	US-08-232-463-14	Sequence 14, Appl
	6	45.2	7.6	22118	3	US-09-815-981A-5	Sequence 5, Appli
c	7	44.6	7.5	614	3	US-09-902-540-1318	Sequence 1318, Ap
c	8	42.4	7.2	1732	3	US-09-270-767-2595	Sequence 2595, Ap
c	9	42.4	7.2	1732	3	US-09-270-767-17877	Sequence 17877, A
c	10	41.8	7.1	601	3	US-09-949-016-142965	Sequence 142965,
c	11	41.8	7.1	601	3	US-09-949-016-142966	Sequence 142966,
c	12	41.8	7.1	601	3	US-09-949-016-142967	Sequence 142967,
	13	41.8	7.1	265038	3	US-09-949-016-15779	Sequence 15779, A
c	14	41.6	7.0	1696	3	US-09-835-811-1	Sequence 1, Appli
	15	41.4	7.0	290	3	US-10-111-827-8418	Sequence 8418, Ap
c	16	41	6.9	612	3	US-09-902-540-1357	Sequence 1357, Ap
c	17	40.8	6.9	2744	3	US-09-071-101-1	Sequence 1, Appli
c	18	40.8	6.9	2744	3	US-09-369-618-1	Sequence 1, Appli
c	19	40.8	6.9	2744	3	US-09-369-617-1	Sequence 1, Appli
c	20	40.2	6.8	2447	2	US-09-014-969-14	Sequence 14, Appl
c	21	40.2	6.8	1030	3	US-09-945-376-3	Sequence 3, Appli
	22	40	6.8	555	3	US-08-905-223-37	Sequence 37, Appl
	23	40	6.8	555	3	US-09-247-155-37	Sequence 37, Appl
	24	40	6.8	555	3	US-09-599-360B-23	Sequence 23, Appl
	25	40	6.8	555	3	US-09-663-600A-37	Sequence 37, Appl
	26	40	6.8	555	3	US-09-621-976-23	Sequence 23, Appl
	27	40	6.8	555	3	US-09-513-999C-23	Sequence 23, Appl
	28	40	6.8	555	3	US-09-471-276-23	Sequence 23, Appl
	29	40	6.8	1039	3	US-09-903-190-37	Sequence 37, Appl
c	30	39.8	6.7	6078	3	US-09-902-540-1280	Sequence 1280, Ap
	31	39.6	6.7	505	3	US-09-173-914-1	Sequence 1, Appli
	32	39.4	6.7	411	3	US-09-621-976-15639	Sequence 15639, A
	33	39.2	6.6	2791	3	US-09-598-401C-30	Sequence 30, Appl
c	34	39.2	6.6	2791	3	US-09-570-367C-1	Sequence 1, Appli
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c	36	39.2	6.6	2240	3	US-09-934-634-1	Sequence 1, Appli
	37	39	6.6	2791	3	US-09-917-278-1	Sequence 1, Appli
	38	39	6.6	2240	3	US-09-814-351-6	Sequence 6, Appli
	39	39	6.6	2240	3	US-09-814-292-1	Sequence 1, Appli
	40	38.8	6.6	6755	3	US-09-814-357-6	Sequence 6, Appli
c	41	38.8	6.6	382	3	US-08-931-999-4	Sequence 4, Appli
c	42	38.8	6.6	515	3	US-09-598-401C-39	Sequence 39, Appl
	43	38.8	6.5	2571	3	US-09-598-401C-84	Sequence 84, Appl
c	44	38.4		1484	3	US-09-598-401C-93	Sequence 93, Appl
	45					US-09-991-181-292	Sequence 292, App

ALIGNMENTS

```
RESULT 1
US-08-725-532A-4
; Sequence 4, Application US/08725532A
; Patent No. 6020179
; GENERAL INFORMATION:
;   APPLICANT: Goli, Surya K.
;   TITLE OF INVENTION:  NOVEL HUMAN TYROSINE PHOSPHATASES
;   NUMBER OF SEQUENCES: 6
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Incyte Pharmaceutical, Inc.
;     STREET:  3174 Porter Drive
;     CITY:  Palo Alto
;     STATE:  CA
;     COUNTRY:  U.S.
;     ZIP:  94304
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Diskette
;     COMPUTER:  IBM Compatible
;     OPERATING SYSTEM:  DOS
;     SOFTWARE:  FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/725,532A
;     FILING DATE:  Filed Herewith
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Billings, Lucy J.
;     REGISTRATION NUMBER:  36,749
;     REFERENCE/DOCKET NUMBER:  PF-0130 US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  415-855-0555
;     TELEFAX:  415-845-4166
; INFORMATION FOR SEQ ID NO:  4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  982 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA
;   IMMEDIATE SOURCE:
;     LIBRARY:
;     CLONE:  Consensus
US-08-725-532A-4

Query Match             52.4%;  Score 310;  DB 3;  Length 982;
Best Local Similarity   100.0%;  Pred. No. 2.7e-77;
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Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  283 TTTGGAGTTGCCCGCTTACTTGGTTGGGTTGGGGGGGGCGGGCGGGGCCTGTTTTGTTCCT 342
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Db  1   TTTGGAGTTGCCCGCTTACTTGGTTGGGTTGGGGGGGGCGGGCGGGGCCTGTTTTGTTCCT 60

Qy  343 TTTCTTTTTAAGAGTTGGGGTTTCTTTTTAATTATCCAAACAGTGGGTGGGTTTTTAAAATCTC 402
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Db  61  TTTCTTTTTAAGAGTTGGGGTTTCTTTTTAATTATCCAAACAGTGGGTGGGTTTTTAAAATCTC 120

Qy  403 CCCACACCCAAGTATTTGCACAATATTTGTGCGGGTATGGGGGTGGGTTTTTAAAATCTC 462
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CCCACACCCAAGTATTTGCACAATATTTGTGCGGGTATGGGGGTGGGTTTTTAAAATCTC 180

Qy  463 GTTTCTTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTGCCCTTCGCGGGGAC 522
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 GTTTCTTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTGCCCTTCGCGGGGAC 240

Qy  523 TTCTCAGGTCGTGTCCCCAGCCTTCTCTGCAGTCCCTTCGCGGGCCCGTCGGG 582
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Qy  583 AGGCGCCATG 592
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Db  301 AGGCGCCATG 310
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RESULT 2
US-09-016-434-993
; Sequence 993, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;   STREET: 3174 PORTER DRIVE
;   CITY: PALO ALTO
;   STATE: CALIFORNIA
;   COUNTRY: USA
;   ZIP: 94304
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/016,434
;   FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Zeller, Karen J.
;   REGISTRATION NUMBER: 37,071
;   REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (650) 855-0555
;   TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 993:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 982 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: STOMTUT01
;   CLONE: 889096

US-09-016-434-993

Query Match 52.4%; Score 310; DB 3; Length 982;
Best Local Similarity 100.0%; Pred. No. 2.7e-77;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db  1   TTTGGAGTTGCCCGCTTACTTGGTTGGGTTGGGGGGGGCGGGCGGGGCCTGTTTTGTTCCT 60

Qy  343 TTTCTTTTTAAGAGTTGGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCC 402
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Db  61  TTTCTTTTTAAGAGTTGGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCC 120

Qy  403 CCCACACCCAAGTATTTGCACAATATTTGTGCGGGTATGGGGGTGGGTTTTTAAAATCTC 462
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Qy  583 AGGCGCCATG 592
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Db  301 AGGCGCCATG 310
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RESULT 3
US-09-164-193-1
; Sequence 1, Application US/09164193C
; Patent No. 6258582
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: NOVEL CSAPTP NUCLEIC ACID MOLECULES AND USES THEREFOR (as amended)
; FILE REFERENCE: MNI-051
; CURRENT APPLICATION NUMBER: US/09/164,193C
; CURRENT FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1315
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (249)..(767)
; FEATURE:
; OTHER INFORMATION: 'n' at position 1315 may be any nucleotide
US-09-164-193-1

Query Match 39.5%; Score 234; DB 3; Length 1315;
Best Local Similarity 100.0%; Pred. No. 7.5e-56;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  359 TGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCCCCACACCCAAGTATT 418
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Db  18  TGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCCCCACACCCAAGTATT 77

Qy  419 TGCACAATATTTGTGCGGGTATGGGGGTGGGTTTTTAAAATCTCGTTTCTTCTTGGACAAG 478
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  78  TGCACAATATTTGTGCGGGTATGGGGGTGGGTTTTTAAAATCTCGTTTCTTCTTGGACAAG 137

Qy  479 CACAGGGATCTCGTTCTCCTCATTTTTGGGGACTTCTCAGGTCGTGTCC 538
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Db  138 CACAGGGATCTCGTTCTCCTCATTTTTGGGGACTTCTCAGGTCGTGTCC 197

Qy  539 CCAGCCTTCTCTGCAGTCCCTTCGCGGGCCGTCGGGAGGCGCCATG 592
        ||||||||||||||||||||||||||||||||||||||||||||||
Db  198 CCAGCCTTCTCTGCAGTCCCTTCGCGGGCCGTCGGGAGGCGCCATG 251
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RESULT 4
US-09-221-448A-1
; Sequence 1, Application US/09221448A
; Patent No. 6436685
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPTP PROTEIN MOLECULES AND USES THEREFOR (AS AMENDED)
; FILE REFERENCE: MNI-051DV1
; CURRENT APPLICATION NUMBER: US/09/221,448A
; CURRENT FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1315
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (249)..(767)
; OTHER INFORMATION: 'n' at position 1315 may be any nucleotide
US-09-221-448A-1

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Query Match            39.5%;  Score 234;  DB 3;  Length 1315;
Best Local Similarity 100.0%;  Pred. No. 7.5e-56;
Matches   234;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    359 TGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCCCCACACCCAAGTATT 418
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Db     18 TGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCCCCACACCCAAGTATT 77

Qy    419 TGCACAATATTTGTGCGGGGTATGGGGGTGGGTTTTTAAATCTCGTTTCTCTTGGACAAG 478
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     78 TGCACAATATTTGTGCGGGGTATGGGGGTGGGTTTTTAAATCTCGTTTCTCTTGGACAAG 137

Qy    479 CACAGGGATCTCGTTCTCCTCATTTTTGGGGGTGTGTGGGGACTTCTCAGGTCGTGTCC 538
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Db    138 CACAGGGATCTCGTTCTCCTCATTTTTGGGGGTGTGTGGGGACTTCTCAGGTCGTGTCC 197

Qy    539 CCAGCCTTCTCTGCAGTCCCTTCTGCCCTGCCGGGCCCGTGCGGAGGGCGCCATG 592
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Db    198 CCAGCCTTCTCTGCAGTCCCTTCTGCCCTGCCGGGCCCGTGCGGAGGGCGCCATG 251
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RESULT 5
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, P.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313

; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pT2gpt-P1s
US-08-232-463-14

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Query Match             8.9%;  Score 52.8;  DB 2;  Length 7218;
Best Local Similarity   3.8%;  Pred. No. 0.00014;
Matches    15;  Conservative 224;  Mismatches 161;  Indels   0;  Gaps   0;

Qy    167 GACACTGCTTGGCGCGGCCGGGTTCACTTGAGTTTTTAAGTTTCTTTGCTGAGCTTTTT 226
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Db   1035 GAGCGTGGCTGCAGGTGCGAGGGAGCTTGCGATYYYYYYYYYYYYYYYYYY 1094

Qy    227 GGTTGTTCTTTTATTTTTGCCTCTTATGACTATCCAGCTCTGAGAGACGGGAGTTG 286
          :  ::::::  :::  ::::  YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY
Db   1095 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1154

Qy    287 GAGTTGCCCGCTTTACTTTGTTGGTTGGGTTGGGGGGGGCGGCGGCCGTGTTTGTTGTTCCTTTC 346
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Qy    347 TTTTTTAAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGGCAGCTTCCTCCCCA 406
          :::::: YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY
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Qy    407 CACCCAAGTATTGCACAATATTGTGCGGGGTATGGGGGTGGGTTTTTAAATCTCGTTT 466
          :  :  ::::  :  ::  ::  ::  :  :::
Db   1275 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1334

Qy    467 CTCTTGGACAAGCACAGGGATCCACAGGGATCTCGTTCTCCTCATTTTTGGGGGTGTGTGGGGACTTCT 526
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Qy    527 CAGGTCGTGTCCCCAGCCTTCTCTGCAGTCCCTTCTGCCC 566
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Db   1395 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1434
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RESULT 6
US-09-815-981A-5
; Sequence 5, Application US/09815981A
; Patent No. 6936469
; GENERAL INFORMATION:
; APPLICANT: de Jong, Gary
; APPLICANT: Vandeby1, Sandra
; TITLE OF INVENTION: METHODS FOR DELIVERING NUCLEIC ACID
; TITLE OF INVENTION: MOLECULES INTO CELLS AND ASSESSMENT THEREOF
; FILE REFERENCE: 24601-416B
; CURRENT APPLICATION NUMBER: US/09/815,981A
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 22118
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-815-981A-5

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Query Match            7.6%;  Score 45.2;  DB 3;  Length 22118;
Best Local Similarity  52.7%;  Pred. No. 0.031;
Matches  98;  Conservative   0;  Mismatches  88;  Indels   0;  Gaps   0;

Qy     192 TTTGAGTTTTTAAGTTTTTCTTGCTGAGCTTTTGGTGTTCTTTTATTTTTGCCTC 251
                |||   |||||| || ||||  ||| |||||||| || ||||||||||
Db   19801 TTTGTTGTTGTTGTTTGTTTGTTTTGTTTGTTTGTTGTTTGTTTTGTTTTGT 19860

Qy     252 TTTATGACTATCCAGCTCTGAGAGACGGAGTTTGGAGTTGCCCGCTTTACTTGGTTGG 311
                |||                                    | |||||| ||||||
Db   19861 TTTGTGTTGTTGTTGTGTGTGTGTTGGGTTGGGTTGGGTTGGGTTGGTTTGGTTGG 19920

Qy     312 GTTGGGGGGGGCGGCGGGCGTGTTTTGTTTTGTTTTCTTTTCTTTTTTAAGAGTTGGGTTTTCTTTT 371
                                 ||| || |||||  |||||||||||||   ||||||
Db   19921 GTTGGGTTGGGTTGGGTTGGTTTTTGTTTGTTTTGGTTTTGTTTGTTTTGGTTTTGGTTTTGTT 19980

Qy     372 TTAATT 377
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Db   19981 TTGTTT 19986


RESULT 7
US-09-902-540-1318/c
; Sequence 1318, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-1015849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1318
; LENGTH: 614
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(614)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1318

Query Match            7.5%;  Score 44.6;  DB 3;  Length 614;
Best Local Similarity  52.4%;  Pred. No. 0.011;
Matches  98;  Conservative   0;  Mismatches  89;  Indels   0;  Gaps   0;

Qy     187 TTCACTTTGAGTTTTTAAGTTTTTCTTGCTGAGCTTTTTGGTGTTCTTTTTATTTTTT 246
                |||  || ||||||||||||||||||||||||||||||||||||||||
Db     462 TTTTTTTTTTTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 403

Qy     247 GCCTCTTTATGACTATCCAGCTCTGAGAGACGGAGTTTGCCCGCTTTACTTTG 306
                ||| |||||||||||
Db     402 TTCTTTTTTTTTTTTGTTTATGTTTTTTGTGTTTTTTTTTTTTATTTT 343

Qy     307 GTTGGGTTGGGGGGGGGCGGCGGCCGTGTTTTCCTTTTTTTTAAGAGTTGGGTTTT 366
                ||||                     |||  ||||||||
Db     342 GTTTTTGTTTTTGTTTTTTTTTGTCTTTTTTTTTGTTTTTTTGTTCT 283

Qy     367 CTTTTTT 373
                |||||||
Db     282 TTTTTTT 276


RESULT 8
US-09-270-767-2595/c
; Sequence 2595, Application US/09270767
; Patent No. 6703491
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; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2595
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-2595

Query Match            7.2%;  Score 42.4;  DB 3;  Length 1732;
Best Local Similarity  50.5%;  Pred. No. 0.068;
Matches 103;  Conservative   0;  Mismatches 101;  Indels   0;  Gaps   0;

Qy     180 GGCCGGGTTCACTTTGAGTTTTTAAGTTTTCTTTGCTGAGCTTTTTTGGTTGGTTGTTCTTTTT 239
                |||                                      |||
Db     554 GGCTGTTTTACATTTAAATGTTTCCTTTTTTTACAGTTCGTTTTTTACAGTTGCTA 495

Qy     240 ATTTTTTTGCCTCTTATGACTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTGCCCGCTT 299
                |||  |||  ||         |||| |  || |||| ||| |||
Db     494 TTTTTTTTGTATTTCGATTTTTGTACGCTATTTATGAATTACTTTGAATTCATTTGCA 435

Qy     300 TACTTTGGTTGGGTTGGGGGGGGCGGCGGGCGTGTTTTTTATTGATTTTTTTTTTAAGAGTT 359
                ||||  |||||||||||
Db     434 TGCTTCGTTTGATTTGGGTTTTATTGATTTTTTTTTGCGTTTTTTTATTTGTAAAATTT 375

Qy     360 GGGTTTTCTTTTTTAATTATCCAA 383
                ||  ||||  |||
Db     374 TTTTTCGGTTTTGCTTTTGTATAA 351


RESULT 9
US-09-270-767-17877/c
; Sequence 17877, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17877
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-17877

Query Match            7.2%;  Score 42.4;  DB 3;  Length 1732;
Best Local Similarity  50.5%;  Pred. No. 0.068;
Matches 103;  Conservative   0;  Mismatches 101;  Indels   0;  Gaps   0;

Qy     180 GGCCGGGTTCACTTTGAGTTTTTAAGTTTTCTTTGCTGAGCTTTTTTGGTTGGTTGTTCTTTTT 239
                |||                                      |||
Db     554 GGCTGTTTTACATTTAAATGTTTCCTTTTTTTACAGTTCGTTTTTTTACAGTTGCTA 495

Qy     240 ATTTTTTTGCCTCTTATGACTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTGCCCGCTT 299
                |||  |||  ||         |||| |  || |||| ||| |||
Db     494 TTTTTTTTGTATTTCGATTTTTGTACGCTATTTATGAATTACTTTGAATTCATTTGCA 435

Qy     300 TACTTTGGTTGGGTTGGGGGGGGCGGCGGGCGTGTTTTTTATTGATTTTTTTTTTAAGAGTT 359
                ||||  |||||||||||
Db     434 TGCTTCGTTTGATTTGGGTTTTATTGATTTTTTTTTTGCGTTTTTTTATTTGTAAAATTT 375

Qy     360 GGGTTTTCTTTTTTAATTATCCAA 383
                ||  ||||  |||
Db     374 TTTTTCGGTTTTGCTTTTGTATAA 351
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RESULT 10
US-09-949-016-142965/c
; Sequence 142965, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 142965
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-142965

Query Match   7.1%; Score 41.8; DB 3; Length 601;
Best Local Similarity 58.4%; Pred. No. 0.066;
Matches   73; Conservative   0; Mismatches 52; Indels   0; Gaps   0;

Qy   183 CGGGTTCACTTTGAGTTTTTAAGTTTTCTTTGCTGAGCTTTTTTGGTTGTTCTTTTTATT 242
           |||||||||||||| |||||| ||||||| ||||| |||||||||||||||||||||||||
Db   364 CGAGGACACTCTGAGTATCTGAGTTTTTGGTTTGGTTGGATTAGCTTTTTTTTTTTTTTTT 305

Qy   243 TTTTGCCTCTTTATGACTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTGCCCGCTTTAC 302
           ||||| ||| |||||||||||||| |||-| ||||||||||||||||||||||||||||
Db   304 TTTTGACAAGGTCTGGCTCTGCCATTCAGGCTGTAGAATAGTGGCGGGATCACAGTTCAC 245

Qy   303 TTTTGG 307
           |||-|
Db   244 TGTAG 240

RESULT 11
US-09-949-016-142966/c
; Sequence 142966, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 142966
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-142966

Query Match   7.1%; Score 41.8; DB 3; Length 601;
Best Local Similarity 58.4%; Pred. No. 0.066;
Matches   73; Conservative   0; Mismatches 52; Indels   0; Gaps   0;

Qy   183 CGGGTTCACTTTGAGTTTTTAAGTTTTCTTTGCTGAGCTTTTTTGGTTGTTCTTTTTATT 242
           |||||||||||||| |||||| ||||||| ||||| |||||||||||||||||||||||||
Db   585 CGAGGACACTCTGAGTATCTGAGTTTTTGGTTTGGTTGGATTAGCTTTTTTTTTTTTTTTT 526

Qy   243 TTTTGCCTCTTTATGACTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTGCCCGCTTTAC 302
           ||||| ||| |||||||||||||| |||-| ||||||||||||||||||||||||||||
Db   525 TTTTGACAAGGTCTGGCTCTGCCATTCAGGCTGTAGAATAGTGGCGGGATCACAGTTCAC 466

Qy   303 TTTTGG 307
           |||-|
Db   465 TGTAG 461

RESULT 12
US-09-949-016-142967/c
; Sequence 142967, Application US/0994916
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 142967
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-142967

Query Match   7.1%; Score 41.8; DB 3; Length 601;
Best Local Similarity 58.4%; Pred. No. 0.066;
Matches   73; Conservative   0; Mismatches 52; Indels   0; Gaps   0;

Qy   183 CGGGTTCACTTGAGTTTTTAAGTTTTCTTTGCTGAGCTTTTTTGGTTGTTCTTTTTATT 242
           ||| ||||| |||||||| |||| ||||||| |||| |||||||||||||||||||||||
Db   589 CGAGGACACTCTGAGTATCTGAGTTTTTGGTTTGGTTGGATTAGCTTTTTTTTTTTTTTTT 530

Qy   243 TTTTGCCTCTTTATGACTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTGCCCGCTTTAC 302
           ||||| ||| |||||||||||||| |||-| ||||||||||||||||||||||||||||
Db   529 TTTTGACAAGGTCTGGCTCTGCCATTCAGGCTGTAGAATAGTGGCGGGATCACAGTTCAC 470

Qy   303 TTTTGG 307
           |||-|
Db   469 TGTAG 465

RESULT 13
US-09-949-016-15779
; Sequence 15779, Application US/0994916
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0

Qy   183 CGGGTTCACTTGAGTTTTTAAGTTTTCTTTGCTGAGCTTTTTTGGTTGTTCTTTTTATT 242

; SEQ ID NO 15779
; LENGTH: 265038
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(265038)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15779

Query Match 7.1%; Score 41.8; DB 3; Length 265038;
Best Local Similarity 58.4%; Pred. No. 0.77;
Matches 73; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 183 CGGGTTCACTTGAGTTTTAAGTTTCTTTGCTGAGCTTTTTGGTTGTTCTTTTATT 242
           |||| ||||| ||||| ||| ||||||| ||||| ||| ||
Db 129123 CGAGGACACTCTGAGTATCTGAGTTTGGTGTTGGATTAGCTTTTTTTTTTTTTTTTTT 129182

Qy 243 TTTTGCCTCTTTATGACTATCCAGCTCTGAGAGACGGAGTTGGAGTTGCCCGCTTAC 302
            ||||| || ||| |||| |||||||| ||| |||| |||||
Db 129183 TTTTGACAAGGTCTGGCTCTGCCATTCAGCTGTGAATAGTGGCGGGATCACAGTTCAC 129242

Qy 303 TTTGG 307
            |||||
Db 129243 TGTAG 129247

RESULT 14
US-09-835-811-1/c
; Sequence No. 1, Application US/09835811
; Patent No. 6482936
; GENERAL INFORMATION:
; APPLICANT: HU, Song et al
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL0012228
; CURRENT APPLICATION NUMBER: US/09/835,911
; CURRENT FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1696
; TYPE: DNA
; ORGANISM: Human
US-09-835-811-1

Query Match 7.0%; Score 41.6; DB 3; Length 1696;
Best Local Similarity 51.0%; Pred. No. 0.11;
Matches 98; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

Qy 198 TTTTTAAGTTTCTTTGCTGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATG 257
           ||||| ||||||| ||||| || |||||| |||||| ||||||
Db 1692 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1633

Qy 258 ACTATCCAGCTCTGAGAGACGGAGTTGGAGTTGCCCGCTTACTTGGTTGGGTTGGG 317
            |||| ||| ||||||||||||||| |||||||||
Db 1632 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1573

Qy 318 GGGGGCGGCGGCGCTGTTTGTTGTTCCTTTCTTTTTTAAGAGTTGGGTTTCTTTTTAATT 377
            |||| |||||||||||| |||||||| |||||
Db 1572 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTA 1513

Qy 378 ATCCAAACAGTG 389
            ||| |||||||
Db 1512 ATCTATACAGTG 1501

RESULT 15
US-10-131-827-8418
; Sequence 8418, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:

; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUN
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 50661200120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8418
; LENGTH: 290
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-8418

Query Match 7.0%; Score 41.4; DB 3; Length 290;
Best Local Similarity 50.8%; Pred. No. 0.064;
Matches 99; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

Qy 199 TTTTAAGTTTCTTTGCTGAGCTTTTTGGTGTTCTTTTATTTTTGCCTCTTTATGA 258
            ||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 60

Qy 259 CTATCCAGCTCTGAGAGACGGAGTTGGAGTTGCCCGCTTACTTGGTTGGGTTGGGG 318
            |||| ||||||||||||||||||||||| ||||||||||
Db 61 TTTTTTTTTTTTTTTTTTTTTTTGGGAGGAGGGGGTGGTTTTTTTTGGGGGGTTAGGG 120

Qy 319 GGGGGCGGCGGCGCTGTTTGTTCCTTTCTTTTTTAAGAGTTGGGTTTCTTTTTAATTA 378
            || ||| || ||| ||||| ||| ||| |||
Db 121 GGAAAAGGGGGGGGATTTTTTTTTTAAGGTTTTTTTTGAAGGGGGGGGTTATTAAAAT 180

Qy 379 TCCAAACAGTGGGCA 393
            ||| |||||||
Db 181 TTGAAAAGGGGGAA 195

Search completed: April 3, 2006, 05:42:46
Job time : 173 secs

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2006, 05:39:30 ; Search time 3204 Seconds
                           (without alignments)
                         10502.910 Million cell updates/sec

Title: US-10-624-670-1
Perfect score: 592
Sequence: 1 ctatagggcacgcgtggtcg.........gcccgtcgggaggcgccatg 592

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 2842172565 3 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :   GenEmbl:*
                1: gb_ba:*
                2: gb_in:*
                3: gb_env:*
                4: gb_om:*
                5: gb_ov:*
                6: gb_pat:*
                7: gb_ph:*
                8: gb_pr:*
                9: gb_ro:*
               10: gb_sts:*
               11: gb_sy:*
               12: gb_un:*
               13: gb_vi:*
               14: gb_htg:*
               15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	557	94.1	2850	6	AX393317	AX393317 Sequence
2	557	94.1	46561	8	AP005888	AP005888 Homo sapi
3	557	94.1	141371	8	AP005792	AP005792 Homo sapi
4	557	94.1	152418	8	AC100803	AC100803 Homo sapi
5	546	92.2	77656	14	AC138743	AC138743 Homo sapi
6	337	56.9	1329	8	BC003105	BC003105 Homo sapi
7	337	56.9	1396	6	CQ827376	CQ827376 Sequence
8	310	52.4	982	6	AR270430	AR270430 Sequence
9	310	52.4	982	6	BD003637	BD003637 Disease a
10	240	40.5	572	6	CQ716903	CQ716903 Sequence
11	240	40.5	572	6	CQ718557	CQ718557 Sequence
12	240	40.5	1006	6	CS113117	CS113117 Sequence
13	240	40.5	1006	8	AF041434	AF041434 Homo sapi
14	234	39.5	1315	6	AR162252	AR162252 Sequence
15	226	38.2	963	8	HSA276554	HSA276554 Homo sapi
16	141.4	23.9	315395	14	AC132017	AC132017 Rattus no
17	131.4	22.2	2291	9	BC066043	BC066043 Mus muscu
18	131.4	22.2	168400	9	AC119884	AC119884 Mus muscu

19	84.2	14.2	232503	14	AC098900	AC098900 Rattus no
20	64.8	10.9	817	9	AF033645	AF033645 Mus muscu
21	54.2	9.2	162934	14	AC139448	AC139448 Rattus no
22	52.8	8.9	7218	6	I66494	I66494 Sequence 14
23	52	8.8	7758	6	AX346005	AX346005 Sequence
24	51.6	8.7	73989	9	AC101573	AC101573 Mus muscu
25	51.6	8.7	213524	14	AC073339	AC073339 Homo sapi
26	51.2	8.6	226454	14	AC162820	AC162820 Bos tauru
27	50.8	8.6	7698	9	AX346602	AX346602 Sequence
28	50.8	8.6	167991	9	AC125175	AC125175 Mus muscu
29	50.8	8.6	213272	14	AC135668	AC135668 Mus muscu
30	50.4	8.4	47722	14	AC113140	AC113140 Homo sapi
31	49.4	8.3	127955	14	AC139907	AC139907 Rattus no
32	49	8.3	202083	14	AC023833	AC023833 Mus muscu
33	48.8	8.3	877	8	HSA325386	AJ325386 Homo sapi
34	48.8	8.2	7721	6	CS105998	CS105998 Sequence
35	48.8	8.2	83296	14	AC022588	AC022588 Homo sapi
36	48.8	8.2	120644	14	AC026496	AC026496 Homo sapi
37	48.6	8.2	4374	6	CS124658	CS124658 Sequence
38	48.6	8.2	5203	6	CQ807142	CQ807142 Sequence
39	48.6	8.2	5203	6	AX795920	AX795920 Sequence
40	48.6	8.2	5203	6	AX822442	AX822442 Sequence
41	48.6	8.2	5203	6	AX826082	AX826082 Sequence
42	48.6	8.2	71532	14	AC023655	AC023655 Homo sapi
43	48.6	8.2	88712	14	AC097315	AC097315 Mus muscu
44	48.6	8.2	349980	6	AX344556	AX344556 Sequence
45	48.4	8.2	173854	14	AC073047	AC073047 Homo sapi

ALIGNMENTS

RESULT 1
AX393317
LOCUS   AX393317   2850 bp   DNA   linear   PAT 23-MAR-2002
DEFINITION Sequence 247 from Patent WO0210217.
ACCESSION   AX393317
VERSION   AX393317.1 GI:19701330
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS   St Croix,B., Kinzler,K.W. and Vogelstein,B.
TITLE   Endothelial cell expression patterns
JOURNAL   Patent: WO 0210217-A 247 07-FEB-2002;
            The Johns Hopkins University (US)
FEATURES   Location/Qualifiers
     source   1..2850
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

ORIGIN
Query Match   94.1%; Score 557; DB 6; Length 2850;
Best Local Similarity   100.0%; Pred. No. 1e-135;
Matches 557; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   36 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTCGGCCCTTGGGGCCTTGGGGCCCACC 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   345 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTCGGCCCTTGGGGCCTTGGGGCCCACC 404

Qy   96 TCTGAGTGAAGGGGCGTGTCTGCCCATCCACCAATGTGGAGAGGGGCGCCCCCGGTGTGGG 155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   405 TCTGAGTGAAGGGGCGTGTCTGCCCATCCACCAATGTGGAGAGGGGCGCCCCCGGTGTGGG 464

Qy   156 GTCCAGCTCTGGACACTGCTTGGCGCGGTTCACTTGAGTTTTTAAGTTTTCTTTGC 215
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   465 GTCCAGCTCTGGACACTGCTTGGCGCGGTTCACTTGAGTTTTTAAGTTTTCTTTGC 524

Qy   216 TGAGCTTTTTTGTTGTTCTTTTATTTTTGCTCTTTTATGACTATCCAGCTCTGAGAG 275

```
Db   525  TGAGCTTTTTGGTTGTTCTTTTTATTTTTGCCTCTTTTGATGACTATCCAGCTCTGAGAG  584
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   276  ACGGGAGTTTGGAGTTGCCCGCTTTACTTTGGTTGGGTTGGGTTGGGGG...          335
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   585  ACGGGAGTTTGGAGTTGCCCGCTTTACTTTGGTTGGGTTGGGTTGGGGGCGCGGGCTGTTT  644
Qy   336  TGTTCCTTTTCTTTTTTAAGAGAGTTGGGTTTCTTTTTTAA.TATCCAAACAGTGGGCAGC  395
          ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db   645  TGTTCCTTTTCTTTTTTAAGAGAGTTGGGTTTCTTTTTTAATTATCCAAACAGTGGGCAGC  704
Qy   396  TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGTATGGGGTGGGTTTTT      455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   705  TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGTATGGGGTGGGTTTTT      764
Qy   456  AAATCTCGTTTCTCCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTTGGGGTGTG   515
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   765  AAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTTGGGGTGTG   824
Qy   516  TGGGGACTTCTCAGGTCGTGTCCCAGCCTTCTTCTGCAGTCCCTTCTGCCCGCGGCC      575
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Db   825  TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTTCTGCAGTCCCTTCTGCCCTGCCCGGGCC  884
Qy   576  CGTCGGGAGGCGCCATG  592
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Db   885  CGTCGGGAGGCGCCATG  901
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RESULT 2
AP005888

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LOCUS       AP005888      46561 bp    DNA     linear   PRI 29-NOV-2002
DEFINITION  Homo sapiens genomic DNA, chromosome 8q24.3, clone: KB1897C9,
            complete sequence.
ACCESSION   AP005888
VERSION     AP005888.3  GI:25901050
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shimizu,N. and Asakawa,S.
  TITLE     Homo sapiens DNA chromosome 8 SEQUENCE
  JOURNAL   Published Only in Database (2002)
REFERENCE   2  (bases 1 to 46561)
  AUTHORS   Shimizu,N. and Asakawa,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-NOV-2002) Nobuyoshi Shimizu, Keio University, School
            of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo
            160-8582, Japan (E-mail:nshimizu@dmb.med.keio.ac.jp,
            Tel:81-3-3351-2370, Fax:81-3-3351-2370)
COMMENT     On Nov 28, 2002 this sequence version replaced gi:25188175.
FEATURES             Location/Qualifiers
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Query Match    94.1%;   Score 557;  DB 8;  Length 46561;
Best Local Similarity  100.0%;   Pred. No. 1.2e-135;
Matches 557;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy       96 TCTGAGTGAAGGGGCTGTCTGCCCATCCACCAATGTGGAGAGGCGCCCCGTGTGGG 155
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Db     8519 GTCCAGCTCTGGACACTGCTTGGGCGGCCGGGTTCACTTTGAGTTTTCTTTGC 8578

Qy      216 TGAGCTTTTTTGGTTGTTCTTTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG 275
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Qy      276 ACGGGAGTTGGAGTTGCCCGCTTACTTTGGTTGGGTTGGGGGGGCCGCGGGCTGTTT 335
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Db     8639 ACGGGAGTTGGAGTTGCCCGCTTACTTTGGTTGGGTTGGGGGGGCCGCGGGCTGTTT 8698

Qy      336 TGTTCCTTTCTTTTTAAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGC 395
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Db     8699 TGTTCCTTTCTTTTTAAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGC 8758

Qy      396 TTCCTCCCCACACCCAGTATTTGCACAATATTGTCGGGGTATGGGGGTGGTTTTT 455
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Qy      456 AAATCTCGTTTCTTGGACAAGCACAGGGATCCGTTCCTCCTCATTTTTGGGGTGTG 515
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Qy      516 TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTCGAGTCCCTTCCTGCCGGGCC 575
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Db     8879 TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTCGAGTCCCTTCCTGCCGGGCC 8938

Qy      576 CGTCGGGAGGCGCCATG 592
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Db     8939 CGTCGGGAGGCGCCATG 8955


RESULT 3
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LOCUS       AP005792      141371 bp    DNA     linear   PRI 25-MAR-2003
DEFINITION  Homo sapiens genomic DNA, chromosome 8q24, clone: KB1533H12,
            complete sequence.
ACCESSION   AP005792
VERSION     AP005792.5  GI:29170597
KEYWORDS    
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shimizu,N. and Asakawa,S.
  TITLE     Homo sapiens DNA chromosome 8 SEQUENCE
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JOURNAL    Published Only in Database (2002)
REFERENCE  2 (bases 1 to 141371)
AUTHORS    Shimizu,N. and Asakawa,S.
TITLE      Direct Submission
JOURNAL    Submitted (27-SEP-2002) Nobuyoshi Shimizu, Keio University, School
           of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo
           160-8582, Japan (E-mail:nshimizu@dmb.med.keio.ac.jp,
           Tel:81-3-3351-2370,.Fax:81-3-3351-2370)
COMMENT    On Mar 24, 2003 this sequence version replaced gi:28971758.
FEATURES             Location/Qualifiers
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Best Local Similarity  100.0%;   Pred. No. 1.3e-135;
Matches  557;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy       36 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGGCCCTTGGGGGCTTGGGGCCCACC 95
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Qy      156 GTCCAGCTCTGGACACTGCTTGGCGGCCGGCGGCGGGGTTCACTTTGAGTTTTTCTTTGC 215
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Qy      216 TGAGCTTTTTTGGTTGTTCTTTTCTTTTTTTGCCCTCTTTATGACTATCCAGCTCTGAGAG 275
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Qy      336 TGTTCCTTTCTTTTTAAGAGTTGGGTTTCTTTTTCTTTTAATTATCCAAACAGTGGGCAGC 395
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Qy      456 AAATCTCGTTCTCTTGACAAGCACAGAGGATCTCGTTCTCCTCATTTTTGGGGTGTG 515
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Qy      516 TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTCTGCAGTCCCTTCTGCCCGCCGGCC 575
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Db   120134 TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTCTGCAGTCCCTTCTGCCCGCCGGCC 120193

Qy      576 CGTCGGGAGGCGCCATG 592
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Db   120194 CGTCGGGAGGCGCCATG 120210
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RESULT 4
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LOCUS        AC100803           152418 bp     DNA      linear    PRI 20-MAY-2003
DEFINITION   Homo sapiens chromosome 8, clone CTD-3064M3, complete sequence.
ACCESSION    AC100803
VERSION      AC100803.11  GI:30911142
KEYWORDS     HTG.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE    1  (bases 1 to 152418)
  AUTHORS    Birren,B., Nusbaum,C. and Lander,E.
  TITLE      Homo sapiens chromosome 8, clone CTD-3064M3
  JOURNAL    Unpublished
REFERENCE    2  (bases 1 to 152418)
  AUTHORS    Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
             Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
             Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
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             Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
             Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
             Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
             Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE      Direct Submission
  JOURNAL    Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome
             Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE    3  (bases 1 to 152418)
  AUTHORS    Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
             Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
             Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
             Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
             Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
             Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
             Graham,J., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
             Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
             Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
             Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,
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             Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
             Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
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           Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
           Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
           Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
TITLE      Direct Submission
JOURNAL    Submitted (10-APR-2003) Whitehead Institute/MIT Center for Genome
           Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE  4  (bases 1 to 152418)
AUTHORS    Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
           Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
           Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
           Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
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           Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
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           Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
           Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
           Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
           Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
           Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
TITLE      Direct Submission
JOURNAL    Submitted (20-MAY-2003) Whitehead Institute/MIT Center for Genome
           Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT    On May 20, 2003 this sequence version replaced gi:29501910.
           All repeats were identified using RepeatMasker:
           Smit, A.F.A. & Green, P. (1996-1997)
           http://ftp.genome.washington.edu/RM/RepeatMasker.html
           -------- Genome Center
               Center: Whitehead institute/ MIT Center for Genome Research
               Center code: WIBR
               Web site: http://www-seq.wi.mit.edu
               Contact: sequence_submissions@genome.wi.mit.edu
           ---------- Project Information
               Center project name: L21447
               Center clone name: 3064_M_3
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           Only the last 152.4 kilobases of this clone are being submitted.
           The reminder overlaps either accession number AC011676 [WICGR
project L30811] or accession number AC138647 [WICGR project L29199].
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Best Local Similarity  100.0%;  Pred. No. 1.3e-135;
Matches 557;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy       276  ACGGGAGTTGGAGTTGCCCGCTTTACTTGGTTGGGTTGGGTGGGGGGGCGGCGGGGCTGTT 335
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Qy       516  TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTCTGCAGTCCCTTCTGCCCCTGCCGGCC   575
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Qy       576  CGTCGGGAGGCGCCATG      592
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DEFINITION  Homo sapiens chromosome 8 clone RP13-994N10 map 8, LOW-PASS
            SEQUENCE SAMPLING.
ACCESSION   AC138743
VERSION     AC138743.1  GI:27764716
KEYWORDS    HTG; HTGS PHASE0.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 77656)
AUTHORS     Birren,B., Nusbaum,C. and Lander,E.
TITLE       Homo sapiens chromosome 8, clone RP13-994N10
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 77656)
AUTHORS     Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
            Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B.,
            Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
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            Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
            Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J.,
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            Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
            Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
            Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R.,
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            Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X.,
            Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
TITLE       Direct Submission
JOURNAL     Submitted (16-JAN-2003) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
            All repeats were identified using RepeatMasker:
            Smit,A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
COMMENT     ------------------- Genome Center
            Center: Whitehead Institute/ MIT Center for Genome Research
            Center code: WIBR
            Web site: http://www-seq.wi.mit.edu
            Contact: sequence_submissions@genome.wi.mit.edu
            -------------------- Project Information
            Center project name: L29168
            Center clone name: 994_N_10

        *  NOTE: This record contains 72 individual
        *  sequencing reads that have not been assembled into
        *  contigs. Runs of N are used to separate the reads
        *  and the order in which they appear is completely
        *  arbitrary. Low-pass sequence sampling is useful for
        *  identifying clones that may be gene-rich and allows
        *  overlap relationships among clones to be deduced.
        *  However, it should not be assumed that this clone
        *  will be sequenced to completion. In the event that
        *  the record is updated, the accession number will
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Qy      96 TCTGAGTGAAGGGGCTGTGTCTGCCCATCCACCAATGTGGAGAGGGGCGCCCCCGTGTGGG 155
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Qy     216 TGAGCTTTTTTGGTTGTTCTTTTATTTTGTCCTCTTTATGACTATCCAGCTCTGAGAG 275
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Qy     336 TGTTCCTTTCTTTTCTTTTTAAGAGTGGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGC 395
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Qy     396 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTCGGGGTATGGGGGTG-GGTTTT 454
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Db   20023 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTCGGGGTATGGGGGTGAGGTTTT 20082

Qy     455 TAAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTCGGGGGTGT 514
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   20083 TAAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTCGGGGGTGT 20142

Qy     515 GTGGGGACTTCTCAGGTCGTGTCCCCAGCCCTTCCCTTCCCTTCTGCCCTTGCCGGGGC 574
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   20143 GTGGGGACTTCTCAGGTCGTGTCCCCAGCCCTTCCCTTCCCTTCTGCCCTTGCCGGGGC 20202

Qy     575 CCGTCGGGAGGGCGCCATG 592
           |||||||||||||||||||
Db   20203 CCGTCGGGAGGGCGCCATG 20220


RESULT 6
BC003105
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LOCUS       BC003105              1329 bp    mRNA    linear    PRI 29-JUN-2004
DEFINITION  Homo sapiens protein tyrosine phosphatase type IVA, member 3,
            transcript variant 2, mRNA (cDNA clone MGC:1950 IMAGE:3357244),
            complete cds.
ACCESSION   BC003105
VERSION     BC003105.1  GI:13311874
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1329)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1329)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
            Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
            Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
            Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
            Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prabhu,
            Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
            Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
            Schein, Asim Siddiqui, Rob Holt, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 6 Row: a Column: 14
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 14589853.
FEATURES             Location/Qualifiers
     source          1..1329
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /clone="MGC:1950 IMAGE:3357244"
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                     /note="synonyms: PRL-3, PRL-R, PRL3"
                     /db_xref="GeneID:11156"
                     /db_xref="MIM:606449"
     CDS             335..781
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                     /codon_start=1
                     /product="protein tyrosine phosphatase type IVA, member 3,
                     isoform 2"
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                     /db_xref="GI:13311875"
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                     /db_xref="MIM:606449"
                     /translation="MARMNRPAPVEVSYKHMRFLITHNPTNATLSTFIEDLKKYGATT
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Query Match                  56.9%;   Score 337;   DB 8;   Length 1329;
Best Local Similarity      100.0%;    Pred. No. 9.5e-78;
Matches    337;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy        256  TGACTATCCAGCTCTGAGAGACGGGAGTTGGGAGTTGCCCGCTTACTTGGTTGGGTTG  315
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Db          1  TGACTATCCAGCTCTGAGAGACGGGAGTTGGGAGTTGCCCGCTTTACTTGGTTGGGTTG   60

Qy        316  GGGGGGGCGGGGGCTGTTTTGTCCTTTCTTTTTCCTTTTCTTTTTAAGAGTTGGGTTTCTTTTTTAA  375
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61  GGGGGGGCGGGGGCTGTTTGTTTCCTTTCTTTTTCCTTTTCTTTTTAAGAGTTGGGTTTTCTTTTTAA  120

Qy        376  TTATCCAAACAGTGGCAGCTTCCTCCCCACACCCAAGTATTGCACAATATTTGTGCG  435
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121  TTATCCAAACAGTGGCAGCTTCCTCCCCCACACCCAAGTATTGCACAATATTTGTGCG  180

Qy        436  GGGTATGGGGTGGGTTTTAAAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCT  495
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181  GGGTATGGGGTGGGTTTTTAAAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCT  240

Qy        496  CCTCATTTTTTGGGGTGTGTGGGGACTTCCAGTCGTGTCCCCAGCCTTCCTCGCAGT  555
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241  CCTCATTTTTTGGGGTGTGTGGGGACTTCCAGTCGTGTCCCCAGCCTTCCTCGCAGT  300

Qy        556  CCCTTCTGCCCCTGCCGGCCCGTCGGGAGGGCCATG  592
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Db        301  CCCTTCTGCCCCTGCCGGCCCGTCGGGAGGGCGCCATG  337
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RESULT 7
CQ827376
LOCUS       CQ827376               1396 bp    DNA     linear    PAT 29-JUN-2004
DEFINITION  Sequence 9 from Patent WO2004050117.
ACCESSION   CQ827376
VERSION     CQ827376.1  GI:49455856
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Meise,M., Bulenberg,K., Nguyen,T. and Tsetsenis,T.
  TITLE     Proteins involved in the regulation of energy homeostasis
  JOURNAL   Patent: WO 2004050117-A 9 17-JUN-2004;
            DeveloGen Aktiengesellschaft fuer entwicklungsbiologische Forschung
            (DE)
FEATURES             Location/Qualifiers
     source          1..1396
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ORIGIN

Query Match   56.9%;   Score 337; DB 6; Length 1396;
Best Local Similarity 100.0%; Pred. No. 9.6e-78;
Matches 337; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   256 TGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGCCCGCTTACTTGGTTGGGTTG 315
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Qy   316 GGGGGGGCGGCGGGGCGCTGTTTGTTCCTTTCTTTTTAAGAGTTGGGTTTCTTTTTAA 375
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GGGTATGGGGGTGGGTTTGGGTTTTTCTTTTTTCTTTTTAAGAGTTGGGTTTCTTTTTAA 120

Qy   376 TTATCCAAACAGTGGGCAGCTTCCTCCCCACACCCAGTATTTGCACAATATTTGTGCG 435
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TTATCCAAACAGTGGGCAGCTCCCACACCCACCCAGTATTTGCACAATATTTGTGCG 180

Qy   436 GGGTATGGGGGTGGGTTTTTAAATCTCGTTTCTTGACAAGCACAGGGATCTCGTTCT 495
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGGTATGGGGGTGGGTTTTTAAATCTCGTTTCTTGACAAGCACAGGGATCTCGTTCT 240

Qy   496 CCTCATTTTTTGGGGTGTGTGGGGACTTCTCAGTCGTGTCCCCAGCCTTCTCTGCAGT 555
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CCTCATTTTTTGGGGTGTGTGGGGACTTCTCAGTCGTGTCCCCAGCCTTCTCTGCAGT 300

Qy   556 CCCTTCTGCCCTGCCCGGCCCGTCGGGAGGCGCCATG 592
           |||||||||||||||||||||||||||||||||||||
Db   301 CCCTTCTGCCCTGCCCGGCCCGTCGGGAGGCGCCATG 337

RESULT 8
AR270430
LOCUS   AR270430   982 bp   DNA   linear   PAT 10-APR-2003
DEFINITION   Sequence 993 from patent US 6500938.
ACCESSION   AR270430
VERSION   AR270430.1   GI:29701664
KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown.
              Unclassified.
REFERENCE   1 (bases 1 to 982)
AUTHORS   Au-Young,J. and Seilhamer,J.J.
TITLE   Composition for the detection of signaling pathway gene expression
JOURNAL   Patent: US 6500938-A 993 31-DEC-2002;
              Incyte Genomics, Inc.; Palo Alto, CA;
              WOX;
FEATURES   Location/Qualifiers
source   1..982
              /organism="unknown"
              /mol_type="genomic DNA"
ORIGIN

Query Match   52.4%;   Score 310; DB 6; Length 982;
Best Local Similarity 100.0%; Pred. No. 1.2e-70;
Matches 310; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   283 TTTGGAGTTGCCCGCTTACTTGGTTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCC 342
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Db   1 TTTGGAGTTGCCCGCTTACTTGGTTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCC   60

Qy   343 TTTCTTTTTAAGAGTTGGGTTTCTTTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCC 402
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TTTCTTTTTAAGAGTTGGGTTTCTTTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCC 120

Qy   403 CCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGGTGGGTTTTTAAATCTC 462
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Db   121 CCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGGTGGGTTTTTAAATCTC 180

Qy   463 GTTTCTTGGACAAGCACAGGGATCTCGTTTCTTGACAAGCACAGGGATCTCGTTTCTTGG 522
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Db   181 GTTTCTTGGACAAGCACAGGGATCTCGTTTCTTGACAAGCACAGGGATCTCGTTTCTTGG 240

Qy   523 TTCTCAGTCGTGTCCCCAGCCTTCTCTGCAGTCGTCCCCAGCCTTCTCTGCAGTCGTCGGG 582
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Db   241 TTCTCAGTCGTGTCCCCAGCCTTCTCTGCAGTCGTCCCCAGCCTTCTCTGCAGTCGTCGGG 300

Qy   523 TTCTCAGTCGTGTCCCCAGCCTTCTCTGCAGTCCTCCCCTGCCCGGCCCGTCGGG 582
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Db   241 TTCTCAGTCGTGTCCCCAGCCTTCTCTGCAGTCCTCCCCTGCCCGGCCCGTCGGG 300

Qy   583 AGGCGCCATG 592
           ||||||||||
Db   301 AGGCGCCATG 310

RESULT 9
BD003637
LOCUS   BD003637   982 bp   DNA   linear   PAT 31-JAN-2002
DEFINITION   Disease associated protein tyrosine phosphatases.
ACCESSION   BD003637
VERSION   BD003637.1   GI:18631598
KEYWORDS   JP 2001501823-A/2.
SOURCE   unidentified
ORGANISM   unidentified
              unclassified.
REFERENCE   1 (bases 1 to 982)
AUTHORS   Gori,S.K.
TITLE   Disease associated protein tyrosine phosphatases
JOURNAL   Patent: JP 2001501823-A 2 13-FEB-2001;
              INSITE PHARMACEUTICALS INC
COMMENT   OS Unidentified
              PN JP 2001501823-A/2
              PD 13-FEB-2001
              PF 02-OCT-1997 JP 199851691Z
              PR 03-OCT-1996 US 08/725532
              PI SURYA K GORI
              PC
              C12N15/09,A61K31/711,A61K38/46,A61K39/395,A61K45/00, PC
              A61K48/00,
              PC A61P11/00,A61P13/08,A61P13/10,A61P15/08,A61P19/02,A61P25/00,
              PC A61P29/00,
              PC A61P29/00,A61P35/00,A61P43/00,C07K16/40,C12N1/19,C12N1/19, PC
              C12N1/21,
              PC C12N5/10,C12N9/16//C12P21/08,C12N15/00,C12N5/00,A61K37/54 CC
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FT   source   1..982
FT   /organism='Unidentified'.
FEATURES   Location/Qualifiers
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ORIGIN

Query Match   52.4%;   Score 310; DB 6; Length 982;
Best Local Similarity 100.0%; Pred. No. 1.2e-70;
Matches 310; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   283 TTTGGAGTTGCCCGCTTACTTTGGTTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCCT 342
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Qy   343 TTTCTTTTTAAGAGTTGGTTTCTTTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCC 402
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TTTCTTTTTAAGAGTTGGTTTCTTTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCC 120

Qy   403 CCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGGTGGGTTTTTAAATCTC 462
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Db   121 CCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGGTGGGTTTTTAAATCTC 180

Qy   463 GTTTCTTGGACAAGCACAGGGATCTCGTTTCTTGACAAGCACAGGGATCTCGTTTCTTGGGAC 522
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Db   181 GTTTCTTGGACAAGCACAGGGATCTCGTTTCTTGACAAGCACAGGGATCTCGTTTCTTGGGAC 240

Qy   523 TTCTCAGTCGTGTCCCCAGCCTTCTCTGCAGTCCCCAGCCTTCTCTGCAGTCGTCGGG 582
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Db   241 TTCTCAGTCGTGTCCCCAGCCTTCTCTGCAGTCCCCAGCCTTCTCTGCAGTCGTCGGG 300

Qy   583 AGGCGCCATG 592
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Db   301 AGGCGCCATG 310

RESULT 10
CQ716903
LOCUS   CQ716903   572 bp   DNA   linear   PAT 03-FEB-2004
DEFINITION   Sequence 2837 from Patent WO02068579.
ACCESSION   CQ716903
VERSION   CQ716903.1 GI:42277760
KEYWORDS   .
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE   1
AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE   Kits, such as nucleic acid arrays, comprising a majority of
               humanexons or transcripts, for detecting expression and other uses
               thereof
JOURNAL   Patent: WO 02068579-A 2837 06-SEP-2002;
               PE Corporation (NY) (US)
FEATURES   Location/Qualifiers
source   1..572
               /organism="Homo sapiens"
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ORIGIN

Query Match   40.5%; Score 240; DB 6; Length 572;
Best Local Similarity 100.0%; Pred. No. 3.4e-52;
Matches   240; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   353 AAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCCCCCACACCCA 412
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Qy   413 AGTATTTGCACAATATTTGTGCGGGTATGGGGGTGGTTTTTAAATCTCGTTTCTCTTG 472
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Db   61 AGTATTTGCACAATATTTGTGCGGGTATGGGGGTGGTTTTTAAATCTCGTTTCTCTTG 120

Qy   473 GACAAGCACAGGGATCTCGTTCCTCCTCATTTTTGGGGTGTGTGGGGACTTCTCAGGTC 532
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Db   121 GACAAGCACAGGGATCTCGTTCCTCCTCATTTTTGGGGTGTGTGGGGACTTCTCAGGTC 180

Qy   533 GTGTCCCCAGCCTTCTCTGCAGTCCCTTCTGCCCTGCCCGGGCCCGTCGGGAGGCGCCATG 592
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GTGTCCCCAGCCTTCTCTGCAGTCCCTTCTGCCCTGCCCGGGCCCGTCGGGAGGCGCCATG 240

RESULT 11
CQ718557
LOCUS   CQ718557   572 bp   DNA   linear   PAT 03-FEB-2004
DEFINITION   Sequence 4491 from Patent WO02068579.
ACCESSION   CQ718557
VERSION   CQ718557.1 GI:42279414
KEYWORDS   .
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE   1
AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE   Kits, such as nucleic acid arrays, comprising a majority of
               humanexons or transcripts, for detecting expression and other uses
               thereof
JOURNAL   Patent: WO 02068579-A 4491 06-SEP-2002;
               PE Corporation (NY) (US)
FEATURES   Location/Qualifiers
source   1..572

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ORIGIN

Query Match   40.5%; Score 240; DB 6; Length 572;
Best Local Similarity 100.0%; Pred. No. 3.4e-52;
Matches   240; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   353 AAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCCCCCACACCCA 412
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 AAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCCCCCACACCCA 60

Qy   413 AGTATTTGCACAATATTTGTGCGGGTATGGGGGTGGTTTTTAAATCTCGTTTCTCTTG 472
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AGTATTTGCACAATATTTGTGCGGGTATGGGGGTGGTTTTTAAATCTCGTTTCTCTTG 120

Qy   473 GACAAGCACAGGGATCTCGTTCCTCCTCATTTTTGGGGTGTGTGGGGACTTCTCAGGTC 532
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GACAAGCACAGGGATCTCGTTCCTCCTCATTTTTGGGGTGTGTGGGGACTTCTCAGGTC 180

Qy   533 GTGTCCCCAGCCTTCTCTGCAGTCCCTTCTGCCCTGCCCGGGCCCGTCGGGAGGCGCCATG 592
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GTGTCCCCAGCCTTCTCTGCAGTCCCTTCTGCCCTGCCCGGGCCCGTCGGGAGGCGCCATG 240

RESULT 12
CS113117
LOCUS   CS113117   1006 bp   DNA   linear   PAT 24-JUN-2005
DEFINITION   Sequence 135 from Patent WO2005054507.
ACCESSION   CS113117
VERSION   CS113117.1 GI:68224689
KEYWORDS   .
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE   1
AUTHORS   Corfe,B. and Chirakkal,H.
TITLE   Gene screen
JOURNAL   Patent: WO 2005054507-A 135 16-JUN-2005;
               University of Sheffield (GB)
FEATURES   Location/Qualifiers
source   1..1006
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               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"
ORIGIN

Query Match   40.5%; Score 240; DB 6; Length 1006;
Best Local Similarity 100.0%; Pred. No. 3.5e-52;
Matches   240; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   353 AAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCCCCCACACCCA 412
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 AAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCCCCCACACCCA 60

Qy   413 AGTATTTGCACAATATTTGTGCGGGTATGGGGGTGGTTTTTAAATCTCGTTTCTCTTG 472
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Db   61 AGTATTTGCACAATATTTGTGCGGGTATGGGGGTGGTTTTTAAATCTCGTTTCTCTTG 120

Qy   473 GACAAGCACAGGGATCTCGTTCCTCCTCATTTTTGGGGTGTGTGGGGACTTCTCAGGTC 532
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GACAAGCACAGGGATCTCGTTCCTCCTCATTTTTGGGGTGTGTGGGGACTTCTCAGGTC 180

Qy   533 GTGTCCCCAGCCTTCTCTGCAGTCCCTTCTGCCCTGCCCGGGCCCGTCGGGAGGCGCCATG 592
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GTGTCCCCAGCCTTCTCTGCAGTCCCTTCTGCCCTGCCCGGGCCCGTCGGGAGGCGCCATG 240

RESULT 13
AF041434

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LOCUS       AF041434          1006 bp    mRNA    linear   PRI 09-AUG-1998
DEFINITION  Homo sapiens potentially prenylated protein tyrosine phosphatase
            hPRL-3 mRNA, complete cds.
ACCESSION   AF041434
VERSION     AF041434.1  GI:3406429
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1006)
  AUTHORS   Zeng,Q., Tan,Y.H. and Hong,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JAN-1998) Membrane Biology laboratory, Institute of
            Molecular and Cell Biology, 30 Medical Drive, Singapore 117609,
            Singapore
FEATURES             Location/Qualifiers
     source          1..1006
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     CDS             238..759
                     /note="potentially prenylated protein tyrosine
                     phosphatase"
                     /codon_start=1
                     /product="hPRL-3"
                     /protein_id="AAC29314.1"
                     /db_xref="GI:3406430"
                     /translation="MARMNRPAPVEVSYKHMRFLITHNPTNATLSTFIEDLKKYGATT
                     VVRVCEVTYDKTPLEKDGITVVDWPFDDGAPPGKVVEDWLSLVKAKFCEAPGSCVAV
                     HCVAGLGRAPVLVALALIESGMKYEDAIQFIRQKRRGRINSKQLTYLEKYRPKQRLRF
                     KDPHTHKTRCCVM"
ORIGIN

Query Match             40.5%;  Score 240;  DB 8;  Length 1006;
Best Local Similarity   100.0%;  Pred. No. 3.5e-52;
Matches  240;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    353 AAGAGTTGGGTTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCCCCACCCA 412
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 AAGAGTTGGGTTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCCCCACCCA 60

Qy    413 AGTATTTGCACAATATTGTGCGGGGTATGGGGTGGGTTTTTAAATCTCGTTTCTCTTG 472
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGTATTTGCACAATATTGTGCGGGGTATGGGGTGGGTTTTTAAATCTCGTTTCTCTTG 120

Qy    473 GACAAGCACAGGGATCGTCGTTCTCCTCATTTTTGGGGGTGTGTGGGGACTTCTCAGGTC 532
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GACAAGCACAGGGATCGTCGTTCTCCTCATTTTTGGGGGTGTGTGGGGACTTCTCAGGTC 180

Qy    533 GTGTCCCAGCCTTCTCTGCAGTCCCTTCTGCCCTGCCCGGCCCGTCGGGAGGCGCCATG 592
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTGTCCCAGCCTTCTCTGCAGTCCCTTCTGCCCTGCCCGGCCCGTCGGGAGGCGCCATG 240


RESULT 14
AR162252
LOCUS       AR162252          1315 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 1 from patent US 6258582.
ACCESSION   AR162252
VERSION     AR162252.1  GI:16229398
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1315)
  AUTHORS   Acton,S.
  TITLE     CSAPTP nucleic acid molecules and uses therefor
  JOURNAL   Patent: US 6258582-A 1 10-JUL-2001;
FEATURES             Location/Qualifiers
     source          1..1315
                     /organism="unknown"
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ORIGIN                                    /mol_type="unassigned DNA"

Query Match             39.5%;  Score 234;  DB 6;  Length 1315;
Best Local Similarity   100.0%;  Pred. No. 1.3e-50;
Matches  234;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    359 TGGGTTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCCCCACCCAAGTATT 418
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Db     18 TGGGTTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCCCCACCCAAGTATT 77

Qy    419 TGCACAATATTGTGCGGGGTATGGGGTGGGTTTTTAAATCTCGTTTCTCTTGGACAAG 478
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     78 TGCACAATATTGTGCGGGGTATGGGGTGGGTTTTTAAATCTCGTTTCTCTTGGACAAG 137

Qy    479 CACAGGGATCGTCGTTCTCCTCATTTTTGGGGGTGTGTGGGGACTTCTCAGTGTGTCC 538
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    138 CACAGGGATCGTCGTTCTCCTCATTTTTGGGGGTGTGTGGGGACTTCTCAGTGTGTCC 197

Qy    539 CCAGCCTTCTCTGCAGTCCCTTCTGCCCTGCCCGGCCCGTCGGGAGGCGCCATG 592
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    198 CCAGCCTTCTCTGCAGTCCCTTCTGCCCTGCCCGGCCCGTCGGGAGGCGCCATG 251


RESULT 15
HSA276554
LOCUS       HSA276554          963 bp    mRNA    linear   PRI 15-DEC-2002
DEFINITION  Homo sapiens mRNA for protein tyrosine phosphatase hPRL-3, short
            form.
ACCESSION   AJ276554
VERSION     AJ276554.1  GI:2698935
KEYWORDS    hPRL-3 gene; protein tyrosine phosphatase hPRL-3.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ievolella,C., Stanchi,F., Pacchioni,B., Silvia,T., Frigimelica,E.,
            Scannapieco,P., Corso,V., Biasio,B. and Lanfranchi,G.
  TITLE     Full-length of some muscular transcripts, Telethon (Italy) project
            B41
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 963)
  AUTHORS   Ievolella,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAR-2000) Ievolella C., CRIBI Biotechnology Centre,
            Universita' di Padova, via G.Colombo 3, 35121, ITALY
COMMENT     splice variant of AF041434.
FEATURES             Location/Qualifiers
     source          1..963
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="8"
                     /map="8q24.3"
                     /tissue_type="skeletal muscle"
                     /tissue_lib="peak8"
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                     /gene="hPRL-3"
     5'UTR           1..223
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     CDS             224..487
                     /gene="hPRL-3"
                     /codon_start=1
                     /product="protein tyrosine phosphatase short form"
                     /protein_id="CAC81757.1"
                     /db_xref="GI:2698936"
                     /db_xref="UniProt/TrEMBL:Q8IVN5"
                     /translation="MARMNRPAPVEVSYKHMRFLITHNPTNATLSTFIEDLKKYEDAI
                     QFIRQKRRGAINSKQLTYLEKYRPKQRLRFKDPHTHKTRCCVM"
     3'UTR           488..963
                     /gene="hPRL-3"
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STS        689..829
           /gene="hPRL-3"
polyA_site 963
           /gene="hPRL-3"
ORIGIN

Query Match    38.2%;  Score 226;  DB 8;  Length 963;
Best Local Similarity  100.0%;  Pred. No. 1.7e-48;
Matches 226;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   367 CTTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCCCCACACCCAAGTATTTGCACAAT 426
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 CTTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCCCCACACCCAAGTATTTGCACAAT 60

Qy   427 ATTTGTGCGGGGTATGGGGGTGGGTTTTTAAATCTCGTTTCTTGGACAAGCACAGGGA 486
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 ATTTGTGCGGGGTATGGGGGTGGGTTTTTAAATCTCGTTTCTTGGACAAGCACAGGGA 120

Qy   487 TCTCGTTCTCCCATTTTTGGGGGTGTGTGGGGACTTCTCAGGTCGTGTCCCCAGCCTT 546
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TCTCGTTCTCCCATTTTTGGGGGTGTGTGGGGACTTCTCAGGTCGTGTCCCCAGCCTT 180

Qy   547 CTCTGCAGTCCCCTTCTGCCCTGCCGGCCCGTCGGGAGCGCCATG 592
         |||||||||||||||||||||||||||||||||||||||||||||
Db   181 CTCTGCAGTCCCCTTCTGCCCTGCCGGCCCGTCGGGAGCGCCATG 226

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Job time : 3210 secs
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2006, 05:39:33 ; Search time 3493 Seconds
(without alignments)
7929.560 Million cell updates/sec

Title: US-10-624-670-1
Perfect score: 592
Sequence: 1 ctataggggcacgcgtggtcg.........gcccgtcgggaggcgccatg 592

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 2339541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	DB ID	Description
1	555.8	93.9	955	5	BX439784	BX439784 BX439784
2	555	93.8	1042	1	AL525371	AL525371 AL525371
3	555	93.8	1046	1	AL541981	AL541981 AL541981
4	545.6	92.2	1009	1	AL530939	AL530939 AL530939
5	545	92.1	956	1	AL542316	AL542316 AL542316
6	532.6	90.0	953	1	AL528298	AL528298 AL528298
7	527.6	89.1	954	1	AL550979	AL550979 AL550979
8	503.6	85.1	868	8	BI767860	BI767860 603060979
9	502	84.8	706	7	CX759082	CX759082 AGENCOURT
10	495.6	83.8	947	1	AL554544	AL554544 AL554544
11	484.2	81.8	932	3	BI771877	BI771877 603055278
12	474.4	80.2	966	5	BU145820	BU145820 AGENCOURT
13	453.6	76.6	904	1	AL549255	AL549255 AL549255
14	453.4	76.6	940	3	BI770311	BI770311 603056215
15	450.8	76.1	861	3	BI834269	BI834269 603084178
16	439.8	74.3	763	2	BI256315	BI256315 602977558
17	398.8	67.4	1002	3	BI488596	BI488596 603021124
18	398.8	67.3	889	1	AL528665	AL528665 AL528665
19	393.8	66.5	1077	6	CD251553	CD251553 AGENCOURT
20	347.8	58.8	944	1	AL523466	AL523466 AL523466
21	327.4	55.3	329	1	CN368835	CN368835 170005999
22	302.6	51.1	886	3	BI754659	BI754659 603025347
23	302.4	51.1	671	3	BI765398	BI765398 603050433
24	295	49.8	321	3	BM721839	BM721839 UI-E-EO-
25	291.6	49.2	1031	5	BQ881257	BQ881257 AGENCOURT
26	291.2	49.2	826	2	BF343031	BF343031 602017143
27	286.2	48.3	900	2	BF342107	BF342107 602012864
28	278.4	47.0	890	2	BE871184	BE871184 601448757
29	274.4	46.4	671	3	BI489974	BI489974 603031739
30	270	45.6	622	7	CR976547	CR976547 CR976547
31	267	45.1	542	7	CR981907	CR981907 CR981907
32	262.6	44.4	946	5	BQ883236	BQ883236 AGENCOURT
33	260.2	44.0	788	3	BI756422	BI756422 603029233
34	253.4	42.8	474	2	BG003094	BG003094 MR3-GN018
35	245.8	41.5	465	2	BG003036	BG003036 MR3-GN018
36	240	40.5	462	1	AA454501	AA454501 zw29f07.r
37	221	37.3	547	2	BE257755	BE257755 601116718
38	211	35.6	647	3	BM791220	BM791220 K-EST0071
39	210.4	35.5	486	8	N40386	N40386 yy01h08.r1
40	198.2	33.5	1086	7	BM551642	BM551642 AGENCOURT
41	196.8	33.2	729	7	CF994511	CF994511 AGENCOURT
42	194	32.8	606	5	BQ638166	BQ638166 hd19c04.y
43	194	32.8	757	5	BM011663	BM011663 60363600?
44	184	31.1	836	2	BF317092	BF317092 601903493
45	155.2	26.2	313	7	CV350134	CV350134 MR2-OT007

ALIGNMENTS

RESULT 1
BX439784
LOCUS   BX439784   955 bp   mRNA   linear   EST 04-MAY-2004
DEFINITION   BX439784 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE014YH13
5-PRIME, mRNA sequence.
ACCESSION   BX439784
VERSION   BX439784.2   GI:47003679
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE   1 (bases 1 to 955)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE   Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On May 15, 2003 this sequence version replaced gi:30775779.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES   Location/Qualifiers
source   1..955
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE014YH13"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
ORIGIN

Query Match   93.9%;   Score 555.8; DB 5; Length 955;
Best Local Similarity   99.5%;   Pred. No. 1.6e-130;
Matches 554; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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                        /db_xref="taxon:9606"
                        /clone="CS0DC011YB02"
                        /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
                        /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
                        /note="1st strand cDNA was primed with a NotI-oligo(dT)
                        primer. Five prime end enriched, double-strand cDNA was
                        digested with Not I and cloned into the Not I and EcoR V
                        sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

     Query Match      93.8%;    Score 555;  DB 1;  Length 1042;
     Best Local Similarity  99.6%;  Pred. No. 2.5e-130;
     Matches 555;  Conservative   1;  Mismatches   1;  Indels   0;  Gaps   0;

Qy   36 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGGCCCTTGGGGCTTGGGGCCCACC 95
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  303 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGGCCCTTGGGGCTTGGGGCCCACC 362

Qy   96 TCTGAGTGAAGGGGCGTGTCGCCCATCCACCAATGTGAGAGAGGCGCCCCCGGTGTGGG 155
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  363 TCTGAGTGAAGGGGCGTGTCGCCCATCCACCAATGTGAGAGAGGCGCCCCCGGTGTGGG 422

Qy  156 GTCCAGCTCTGGACACTGCTTGGCGCCGGGTTCACTTGAGTTTTTCTTTGC 215
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  423 GTCCAGCTCTGGACACTGCTTGGCGCCGGGTTCACTTGAGTTTTTCTTTGC 482

Qy  216 TGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG 275
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  483 TGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG 542

Qy  276 ACGGGAGTTTGGAGTTGCCCGCTTTACTTGGTTGGGGGGCGGCGGGCTGTTT 335
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Db  543 ACGGGAGTATGGAGTTGCCCGCTTTACTTGGTTGGGGGGCGGCGGGCTGTTT 602

Qy  336 TGTTCCTTTTCTTTTTTAAGAGTTGGGTTTCTTTTTCTTTTTTAATTATCCAAACAGTGGCAGC 395
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  603 TGTTCCTTTTCTTTTTTAAGAGTTGGGTTTCTTTTTCTTTTTTAATTATCCAAACAGTGGCAGC 662

Qy  396 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGTGGGGTTTT 455
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Db  663 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGTGGGGTTTT 722

Qy  456 AAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCTCGTTCTCTTCCTCATTTTTTGGGGGTGTG 515
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  723 AAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCTCGTTCTCTTCCTCATTTTTTGGGGGTGTG 782

Qy  516 TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCCTTCTGCAGTCCTTCTGCAGTYCCTTCTGCCCTGCCCGGCC 575
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  783 TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCCTTCTGCAGTCCTTCTGCCCTGCCCGGCC 842

Qy  576 CGTCGGGAGGCGCCATG 592
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Db  843 CGTCGGGAGGCGCCATG 859
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RESULT 3
AL541981
LOCUS   AL541981   1046 bp   mRNA   linear   EST 24-MAR-2004
DEFINITION AL541981 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE007YN08
            5-PRIME, mRNA sequence.
ACCESSION   AL541981
VERSION   AL541981.3 GI:45717557
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 1046)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT   On Feb 15, 2001 this sequence version replaced gi:30546679.

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Qy   36 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGGCCCTTGGGGCTTGGGGCCCACC 95
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Db  301 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGGCCCTTGGGGCTTGGGGCCCACC 360

Qy   96 TCTGAGTGAAGGGGCGTGTCGCCCATCCACCAATGTGAGAGAGGCGCCCCCGGTGTGGG 155
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 TCTGAGTGAAGGGGCGTGTCGCCCATCCACCAATGTGAGAGAGGCGCCCCCGGTGTGGG 420

Qy  156 GTCCAGCTCTGGACACTGCTTGGCGCCGGGTTCACTTGAGTTTTTCTTTGC 215
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 GTCCAGCTCTGGACACTGCTTGGCGCCGGGTTCACTTGAGTTTTTCTTTGC 480

Qy  216 TGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG 275
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Db  481 TGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG 540

Qy  276 ACGGGAGTTTGGAGTTGCCCGCTTTACTTGGTTGGGGGGCGGCGGGCTGTTT 335
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 ACGGGAGTTTGGAGTTGCCCGCTTTACTTGGTTGGGGGGCGGCGGGCTGTTT 600

Qy  336 TGTTCCTTTTCTTTTTTAAGAGTTGGGTTTCTTTTTCTTTTTTAATTATCCAAACAGTGGCAGC 395
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Db  601 TGTTCCTTTTCTTTTTTTAAGAGTTGGGTTTCTTTTTCTTTTTTAATTATCCAAACAGTGGCAGC 660

Qy  396 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGTGGGGTTTT 455
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGTGGGGTTTT 720

Qy  456 AAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCTCGTTCTCTTCCTCATTTTTTGGGGGTGTG 515
        |||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db  721 AAATCTCGTTTCTCTTGGACAARCACAGGGATCTCGTTCTCGTTCTCTTCCTCATTTTTTGGGGGTGTG 780

Qy  516 TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCCTTCTGCAGTCCTTCTGCCCTGCCCGGCC 575
        ||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db  781 TGGGGACTTCTCARGTCGTGTCCCCAGCCTTCCTTCTGCAGTCCTTCTGCCCTGCCCGGCC 840

Qy  576 CGTCGGGAGGCGCCATG 592
        |||||||||||||||||
Db  841 CGTCGGGAGGCGCCATG 857
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RESULT 2
AL525371
LOCUS   AL525371   1042 bp   mRNA   linear   EST 24-MAR-2004
DEFINITION AL525371 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DC011YB02 5-PRIME, mRNA sequence.
ACCESSION   AL525371
VERSION   AL525371.3 GI:45700569
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 1042)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT   Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES   Location/Qualifiers
     source   1..1042
                     /organism="Homo sapiens"
                     /mol_type="mRNA"

Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES   Location/Qualifiers
    source   1..1046
                  /organism="Homo sapiens"
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                  /db_xref="taxon:9606"
                  /clone="CS0DE007YN08"
                  /tissue_type="PLACENTA"
                  /clone_lib="Homo sapiens PLACENTA"
                  /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
                  with a NotI-oligo(dT) primer. Five prime end enriched,
                  double-strand cDNA was digested with Not I and cloned into
                  the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                  Library was not normalized."

ORIGIN

Query Match   93.8%;   Score 555; DB 1; Length 1046;
Best Local Similarity 99.6%; Pred. No. 2.5e-130;
Matches 555; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy   36 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGGCCCTTGGGGCTTGGGGCCCACC 95
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   303 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGGCCCTTGGGGCTTGGGGCCCACC 362

Qy   96 TCTGAGTGAAGGGGCGGGCTGTCTGCCCATCCACCAATGTGGAGAGGGCGCCCCCGGTGTGGG 155
          ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   363 TCTGAGTAAAGGGGCGGGCTGTCTGCCCATCCACCAATGTGGAGAGGGCGCCCCCGGTGTGGG 422

Qy   156 GTCCAGCTCTGGACACTGCTTGGGCGGGCCGGGTTCACTTTGAGTTTTTCTTTGC 215
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   423 GTCCAGCTCTGGACACTGCTTGGGCGGGCCGGGTTCACTTTGAGTTTTTAARTTTTCTTTGC 482

Qy   216 TGAGCTTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG 275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   483 TGAGCTTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG 542

Qy   276 ACGGGAGTTGGAGTTGCCCGCTTACTTGGTTGGGGGTTGGGGGGGCGGCGGCTGTTT 335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   543 ACGGGAGTTGGAGTTGCCCGCTTACTTGGTTGGGGGTTGGGGGGGCGGCGGCTGTTT 602

Qy   336 TGTTCCTTTTCTTTTTTTTAAGAGTTGGGTTTCTTTTTTAATTATCCAAACAGTGGGCAGC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   603 TGTTCCTTTTCTTTTTTTTAAGAGTTGGGTTTCTTTTTTAATTATCCAAACAGTGGGCAGC 662

Qy   396 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGTGGGTTTTT 455
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   663 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGTGGGTTTTT 722

Qy   456 AAATCTCGTTTCTTCTTGGACAAGCACAGGGATCCGTTCTTCCTCATTTTTGGGGGTGTG 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   723 AAATCTCGTTTCTTCTTGGACAAGCACAGGGATCCGTTCTTCCTCATTTTTGGGGGTGTG 782

Qy   516 TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTGCAGTCCCTTGCCCTGCCCGGCC 575
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Db   783 TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTGCAGTCCCTTGCCCTGCCCGGCC 842

Qy   576 CGTCGGGAGGCGGCCATG 592
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Db   843 CGTCGGGAGGCGGCCATG 859

RESULT 4
AL530939
LOCUS   AL530939   1009 bp   mRNA   linear   EST 24-MAR-2004
DEFINITION AL530939 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens

cDNA clone CS0DD003YN11 5-PRIME, mRNA sequence.
ACCESSION   AL530939
VERSION   AL530939.3   GI:45705888
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 1009)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE   Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On Feb 13, 2001 this sequence version replaced gi:31068772.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.

FEATURES   Location/Qualifiers
    source   1..1009.
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="CS0DD003YN11"
                  /tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
                  /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
                  /note="1st strand cDNA was primed with a NotI-oligo(dT)
                  primer. Five prime end enriched, double-strand cDNA was
                  digested with Not I and cloned into the Not I and EcoR V
                  sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match   92.2%;   Score 545.6; DB 1; Length 1009;
Best Local Similarity   99.6%; Pred. No. 6.3e-128;
Matches 556; Conservative 1; Mismatches 0; Indels 0; Gaps 1;

Qy   36 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGGCCCTTGGGGCTTGGGGCCCACC 95
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   303 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGGCCCTTGGGGCTTGGGGCCCACC 362

Qy   96 TCTGAGTGAAGGGGCGGGCTGTCTGCCATCCACCAATGTGGAGAGGGCGCCCCCGGTGTGGG 155
          ||||||||| |||||||||||||||| ::||||||||||||||||||||||||||||||
Db   363 TCTGAGTAAGGGGCGGGCTGTCGYCATCCACCAATGTGGAGAGGGCGCCCCCGGTGTGGG 422

Qy   156 GTCCAGCTCTGGACACTGCTTGGGCGGGCCGGGTTCACTTTGAGTTTTTCTTTGC 215
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   423 GTCCAGCTCTGGACACTGCTTGGGCGGGCCGGGTTCACTTTGAGTTTTTAAGTTTTCTTTGC 482

Qy   216 TGAGCTTTTTGGTGTTCTTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG 275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   483 TGAGCTTTTTGGTGTTCTTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG 542

Qy   276 ACGGGAGTTGGAGTTGCCCGCTTACTTGGTTGGGGGTTGGGGGGGCGGCGGCTGTTT 335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   543 ACGGGAGTTGGAGTTGCCCGCTTACTTGGTTGGGGGTTGGGGGGGCGGCGGCTGTTT 602

Qy   336 TGTTCCTTTTCTTTTTTTTAAGAGTTGGGTTTTTTTTTTAATTATCCAAACAGTGGGCAGC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   603 TGTTCCTTTTCTTTTTTTTAAGAGTTGGGTTTTTTTTTTAATTATCCAAACAGTGGGCAGC 662

Qy   396 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGTGGGTTTTT 455
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   663 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGTGGGTTTTT 722

Qy   456 AAATCTCGTTTCTTCTTGGACAAGCACAGGGATCCGTTCTTCCTCATTTTTTGGGGGTGTG 515
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   723 AAATCTCGTTTCTTCTTGGACAAGCACAGGGATCCGTTCTTCCTCATTTTTTGGGGGTGTG 782

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Qy   516  TGGGACTTCTCAGGTCGTGTCCCAGCCTTCTCTGCAGTCCCTTCTG--CCCTGCGGGC  574
          ||||||||||||||||||||||||||||||||||||||||| |||||   |||||||||
Db   783  TGGGACTTCTCAGGTCGTGTCCCAGCCTTCTCTGCAGTCCCTTCTGYCCCTGCGCCGGGC  842

Qy   575  CGTCGGGAGGCGCCATG  592
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Db   843  CGTCGGGAGGCGCCATG  860
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RESULT 5
AL542316
LOCUS   AL542316   956 bp   mRNA   linear   EST 24-MAR-2004
DEFINITION AL542316 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE010YP23
            5-PRIME, mRNA sequence.
ACCESSION   AL542316
VERSION   AL542316.3 GI:45717892
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 956)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT   On Feb 15, 2001 this sequence version replaced gi:30547347.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was not normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES   Location/Qualifiers
     source   1..956
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DE010YP23"
                     /tissue_type="PLACENTA"
                     /clone_lib="Homo sapiens PLACENTA"
                     /note="vector: pCMVSPORT 6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoR V sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
ORIGIN

Query Match   92.1%; Score 545; DB 1; Length 956;
Best Local Similarity   99.8%; Pred. No. 8.8e-128;
Matches   556; Conservative   0; Mismatches   0; Indels   1; Gaps   1;

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Qy    36  CTGGAGTTGGTTCAGTTCAGTTCATTCTTCCTCTGGCCCTTGGGGGCTTGGGGCCCACC  95
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Db   301  CTGGAGTTGGTTCAGTTCAGTTCATTCTTCCTCTGGCCCTTGGGGGCTTGGGGCCCACC  360

Qy    96  TCTGAGTGAAGGGGCTGTCTGCCATCCACCAATGTGGAGAGGGCGCCCCCGGTGTGGG  155
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  TCTGAGTGAAGGGGCTGTCTGCCATCCACCAATGTGGAGAGGGCGCCCCCGGTGTGGG  420

Qy   156  GTCCAGCTCTGGACACTGCTTGGCGGCCGGCGGTTCACTTGAGTTTTCTTTGC  215
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  GTCCAGCTCTGGACACTGCTTGGCGGCCGGCGGTTCACTTGAGTTTTCTTTGC  480

Qy   216  TGAGCTTTTTGGTTGTTCTTTTATTTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG  275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  TGAGCTTTTTGGTTGTTCTTTTATTTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG  540

Qy   276  ACGGGAGTTTGGAGTTGCCCCGCTTTACTTGGTTGGGTTGGGGGGCGGCGGGGTGTTT  335
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Db   541  ACGGGAGTTTGGAGTTGCCCGGCCTTTACTTGGTTGGGTTGGGGCGGCGGGGGCGTGTTT  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   336  TGTTCCTTTCTTTTTTAAGAGTTGGGTTTCTTTTTCTTTTTTAATTATCCAAACAGTGGCAGC  395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  TGTTCCTTTCTTTTTTAAGAGTTGGGTTTCTTTTTCTTTTTTAATTATCCAAACAGTGGCAGC  660

Qy   396  TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGTATGGGGGTGGGTTTTT  455
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGTATGGGGGTGGGTTTTT  720

Qy   456  AAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCTTCCTCATTTTTTGGGGGTGTG  515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  AAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCTTCCTCATTTTTTGGGGGTGTG  780

Qy   516  TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTCTGCAGTCCCTTCTGCCGCCGGCC  575
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Db   781  TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTCTGCAGTCCCTTCTGCCGCCGGCC  839

Qy   576  CGTCGGGAGGCGCCATG  592
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Db   840  CGTCGGGAGGCGCCATG  856
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RESULT 6
AL528298
LOCUS   AL528298   953 bp   mRNA   linear   EST 24-MAR-2004
DEFINITION AL528298 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DC023YK24 5-PRIME, mRNA sequence.
ACCESSION   AL528298
VERSION   AL528298.3 GI:45703369
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 953)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT   On Feb 13, 2001 this sequence version replaced gi:31066148.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES   Location/Qualifiers
     source   1..953
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DC023YK24"
                     /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match   90.0%; Score 532.6; DB 1; Length 953;
Best Local Similarity   99.5%; Pred. No. 1.3e-124;
Matches   554; Conservative   1; Mismatches   0; Indels   2; Gaps   2;

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Qy    36  CTGGAGTTGGTTCAGTTCAGTTCATTCTTCCTCTGGCCCTTGGGGGCTTGGGGCCCACC  95
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Db   303  CTGGAGTTGGTTCAGTTCAGTTCATTCTTCCTCTGGCCCTTGGGGGCTTGGGGCCCACC  362

Qy    96  TCTGAGTGAAGGGGCTGTCTGCCATCCACCAATGTGGAGAGGGCGCCCCCGGTGTGGG  155
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match   89.1%; Score 527.6; DB 1; Length 954;
Best Local Similarity 98.4%; Pred. No. 2.4e-123;
Matches 549; Conservative 4; Mismatches 3; Indels 2; Gaps 2;

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Qy    36 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGCCCCTTGGGCCCACC  95
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Db   301 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGCCCCTTGGGCCCACC  360

Qy    96 TCTGAGTGAAGGGGGCGTCTCGCCCATCCACCAATGTGGAGAGGGCGCCCC  155
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Db   361 TCTGAGTGAAGGGGGCGTCTCGCCCATCCACCAATGTGGAGAGGGCGCCCC  420

Qy   156 GTCCAGCTCTGGACACTGCTTGGCGGCGGGTTCACTTGAGTTTTTCTTTGC  215
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GTCCAGCTCTGGACACTGCTTGGCGGCGGGTTCACTTGAGTTTTTCTTTGC  480

Qy   216 TGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG  275
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Db   481 TGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG  540

Qy   276 ACGGGAGTTTGGAGTTGCCCGCTTACTTGGTTGGGGGGCGGGGGCTGTTT  335
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Db   541 ACGGGAGTTTGGAGTTGCCCGCTTACTTGGTTGGGGGGCGGGGGCTGTTT  600

Qy   336 TGTTCCTTTTCTTTTTTAAGAGTGGGTTTCTTTTTAATTATCCAAACAGT-GGGCAG  394
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Db   601 TGTTCCTTTTCTTTTTTAAGAGTGGGTTTCTTTTTAATTATCCAAACAGTGGGGCAG  660

Qy   395 CTTCCTCCCCACACCCAAGTATTGCACAATATTGTGCGGGTATGGGGTTTT  454
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTTCCTCCCCACACCCAAGTATTGCACAATATTGTGCGGGTATGGGGTTTT  720

Qy   455 TAAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTTTGGGGGTGT  514
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Db   721 TAAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTTTGGGGGTGT  780

Qy   515 GTGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCCTTCTCTGCAGTCCCTTCTGCCCGGC  574
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GTGGGGACTTCTCAGGKCGTGT-CCCCAGTCTCTTCTCTKCAGTCRCTTCTGYCCTGCCGGTGY  839

Qy   575 CCGTCGGGAGGGCGCCATG  592
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Db   840 CCGTCGGGAGGGCGCCATG  857
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RESULT 8
BI767860
LOCUS   BI767860   868 bp   mRNA   linear   EST 25-SEP-2001
DEFINITION 603060979F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5210323 5',
            mRNA sequence.
ACCESSION   BI767860
VERSION   BI767860.1 GI:15759438
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 868)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be

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Db   363 TCTGAGTGAAGGGGGCGTCTCGCCCATCCACCAATGTGGAGAGGGCGCCCCGGTGTGGG  422
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Qy   156 GTCCAGCTCTGGACACTGCTTGGCGGCGGGTTCACTTGAGTTTTTCTTTGC  215
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Db   423 GTCCAGCTCTGGACACTGCTTGGCGGCGGGTTCACTTGAGTTTTTCTTTGC  482

Qy   216 TGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG  275
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Db   483 TGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG  542

Qy   276 ACGGGAGTTTGGAGTTGCCCGCTTACTTGGTTGGGGGGCGGGGGCTGTTT  335
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Db   543 ACGGGAGTTTGGAGTTGCCCGCTTACTTGGTTGGGGGGCGGGGGCTGTTT  602

Qy   336 TGTTCCTTTTCTTTTTTAAGAGTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGC  395
         ||||||||||||||||||||||||||||||||||||||||
Db   603 TGTTCCTTTTCTTTTTTAAGAGTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGC  662

Qy   396 TTCCTCCCCACACCCAAGTATTGCACAATATTGTGCGGGTATGGGGTTTT  455
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Db   663 TTCCTCCCCACACCCAAGTATTGCACAATATTGTGCGGGTATGGGGTTTT  722

Qy   456 AAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTTTGGGGGTG  515
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   723 AAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTTTGGGGGTG  782

Qy   516 TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCCTTCTCTGCAGTCCCTTCTGCCCGGCC  575
         ||||||||||||||||||||||||||||||||||||||||
Db   783 TGGGGAC-TCTCAGGTCGTGTCCCCAGCCTTCCTTCTCTCATTTCTCTGCCCTG-CGGGCC  840

Qy   576 CGTCGGGAGGGCGCCATG  592
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Db   841 CGTCGGGAGGSGCCATG  857
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RESULT 7
AL550979
LOCUS   AL550979   954 bp   mRNA   linear   EST 25-MAR-2004
DEFINITION AL550979 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI065YD20 5-PRIME, mRNA sequence.
ACCESSION   AL550979
VERSION   AL550979.3 GI:45751340
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 954)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE   Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On Feb 15, 2001 this sequence version replaced gi:31272796.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: segref@genoscope.cns.fr, Web ; www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES   Location/Qualifiers
     source   1..954
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI065YD20"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was

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              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM11527 row: n  column: 20
              High quality sequence stop: 848.
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     source   1..868
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              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:5210323"
              /lab_host="DH10B"
              /clone_lib="NIH_MGC_122"
              /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
              Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
              anonymous pool of 24 week female lung, 16 week female
              spleen, and 20-22 week male spleens. Library is oligo-dT
              primed and directionally cloned (EcoRV site is destroyed
              upon cloning). Average insert size 1.4 kb, insert size
              range 1-3 kb. Library is normalized and enriched for
              full-length clones and was constructed by C. Gruber
              (Invitrogen). Research Genetics tracking code 026. Note:
              this is a NIH_MGC Library."
ORIGIN

Query Match       85.1%;  Score 503.6;  DB 3;  Length 868;
Best Local Similarity  97.8%;  Pred. No. 3.1e-117;
Matches 542;  Conservative  0;  Mismatches  9;  Indels  3;  Gaps  3;

Qy     36 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGGCCCTTGCGGGGCTTGGGGCTCCACC   95
          |||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||
Db    316 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGGCCCTTGGGGGCTTGGGGCCCCACC  375

Qy     96 TCTGAGTGAAGGGGGCTGTCTGCCCATCCACCAATGTGAGAGAGGGGCGCCCCCGGTGTGGG  155
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    376 TCTGAGTGAAGGGGGCTGTCTGCCCATCCACCAATGTGAGAGAGGGGCGCCCCCGGTGTGGG  435

Qy    156 GTCCAGCTCTGGACACTGCTTGGCGGCCGGGTTCACTTGAGTTTTTCTTTGC  215
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    436 GTCCAGCTCTGGACACTGCTTGGCGGCCGGGTTCACTTGAGTTTTTCTTTGC  495

Qy    216 TGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG  275
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    496 TGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG  555

Qy    276 ACGGGAGTTGGAGTTGCCCGCTTTACTTTGGTTGGGTTGGGTTGGGGGGGGGGGGCGGCGGCTGTTT  335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    556 ACGGGAGTTGGAGTTGCCCGCTTTACTTTGGTTGGGTTGGGTTGGGGGGGGGGGGCGGCGGCTGTTT  615

Qy    336 TGTTCCTTTCTTTTTTAAGAGTTGGGTTTTTCTTTTTAATTATCCAAACAGTGGCAGC  395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    616 TGTTCCTTTCTTTTTTAAGAGTTGGGTTTTTCTTTTTAATTATCCAAACAGTGGCAGC  675

Qy    396 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGCGGGT-GGGTTTT  454
          |||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||
Db    676 TTCCTCCCCCAGACCCAAGTATTTGCACAATATTTGTGCGGGGTATGCGGGTATGCGGGTAGGGCTCT  735

Qy    455 TAAATCTCGTTTCTCTTGGACAAGCACAGGGATCCGTTCGTTCTTCATTTTTTGGGGGTGT  514
          |||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db    736 CAAATCTCGTTTCTCTTGGACAAGCACAGCATCCGTTCGTTCTTCTCA-TTTAAGGGGGTGT  794

Qy    515 GTGGGGACTTCTCAGGTCGTGTCCCCAGCGCTTCCCTTCTGCCCTCGGC  574
          ||||||||||||||||||||||||||||||||||||||  |||||||||
Db    795 GTGGGGACTTCTCAGGTCGTGTCCCCCAGGCTTCTCTGCAGTCCCTGCCCTGCGGG-  853

Qy    575 CCGTTCGGGAGGCGGC  588
          ||||||||||||||||
Db    854 CCGTTCGGGAGGCGGC  867

RESULT 9
CX759082
LOCUS        CX759082                 706 bp    mRNA        linear   EST 24-JAN-2005
DEFINITION   AGENCOURT_41357736 NIH_MGC_279 Homo sapiens cDNA clone
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ACCESSION    CX759082
VERSION      CX759082.1  GI:58055738
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE    1  (bases 1 to 706)
  AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
             National Institutes of Health, Mammalian Gene Collection (MGC)
  TITLE      Unpublished (1999)
  JOURNAL    Office of Cancer Genomics
             National Cancer Institute / NIH
             Bldg. 31 Rm10A07 Bethesda, MD 20892
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Meri Pirpo
             cDNA Library Preparation: Express Genomics
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
  COMMENT    Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLAM15921 row: 1  column: 15
             High quality sequence stop: 677.
FEATURES     Location/Qualifiers
     source  1..706
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             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="IMAGE:7775009"
             /tissue_type="pluripotent cell line derived from
             blastocyst inner cell mass"
             /lab_host="DH10B TonA"
             /clone_lib="NIH_MGC_279"
             /note="Organ: Blastocyst; Vector: pExpress-1; Site_1:
             EcoRV; Site_2: NotI; RNA obtained from pluripotent cell
             line derived from blastocyst inner cell mass (cell line
             HSF-1.14, NIH Registry designation UC01. Positive for OCT4
             expression by rtPCR; positive for SSEA-3, SSEA-4,
             Tra-1-81, Tra-1-60 by immunofluorescence. Negative for
             SSEA-1 by immunofluorescence. Passage 35. This line is a
             subclone of the parental line; the parental line was
             subcloned to remove aneuploid cells). cDNA was primed
             using oligo-dT primer:
             5'-pGACTAGTTCTAGATCGCGAGCGGCGCGCCC(T)25-3' and cloned into
             the EcoRV/NotI sites of pExpress-1. Size-selection >1.25
             kb resulted in an average insert size of 1.82 kb. This
             primary library is normalized (non-normalized primary
             library is NIH_MGC_278) and was constructed by Express
             Genomics (Frederick, MD). Note: this is a Mammalian Gene
             Collection library."
ORIGIN

Query Match       84.8%;  Score 502;  DB 8;  Length 706;
Best Local Similarity  100.0%;  Pred. No. 7.5e-117;
Matches 502;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     91 CCACCTCTGAGTGAAGGGGGCTGTCTGCCCATCCACCAATGTGAGAGAGGGGCGCCCCCGGT  150
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCACCTCTGAGTGAAGGGGGCTGTCTGCCCATCCACCAATGTGAGAGAGGGGCGCCCCCGGT   60

Qy    151 GTGGGGTCCAGCTCTGGACACTGCTTGGCGGCCGGGTTCACTTGAGTTTTTAAGTTTTC  210
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GTGGGGTCCAGCTCTGGACACTGCTTGGCGGCCGGGTTCACTTGAGTTTTTAAGTTTTC  120

Qy    211 TTTGCTGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATGACTATCCAGCTCT  270
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TTTGCTGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATGACTATCCAGCTCT  180

Qy    271 GAGAGACGGGAGTTGGAGTTGCCCGCTTTACTTTGGTTGGGTTGGGGGGGGGGGGGGC  330
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Db  181 GAGAGACGGGAGTTGGAGTTGCCCGCTTAAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGG 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  331 TGTTTTGTTGTTCCTTTTCTTTTTTCTTTTTTTTTAAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGG 390
        |||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db  241 TGTTTTGTTCTTTTCTTTTTTCTTTTTTTTTAAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGG 300

Qy  391 GCAGCTTCCTCCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGTATGGGGGTGGG 450
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 GCAGCTTCCTCCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGTATGGGGGTGGG 360

Qy  451 TTTTAAATCTCGTTTCTCTTGACAAGCACAGGGATCCGTTCTCCTCATTTTTTGGGG 510
        |||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db  361 TTTTAAATCTCGTTTCTCTTGACAAGCACAGGGATCCGTTCTCCTCATTTTTTGGGG 420

Qy  511 GTGTGTGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTCTGCAGTCCCTTGCCCTGCC 570
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 GTGTGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTCTGCAGTCCCTTGCCCTGCC 480

Qy  571 GGGCCCGTCGGGAGGCGCCATG 592
        ||||||||||||||||||||||
Db  481 GGGCCCGTCGGGAGGCGCCATG 502
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RESULT 10
AL554544
LOCUS   AL554544   947 bp   mRNA   linear   EST 30-MAR-2004
DEFINITION AL554544 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
           clone.CS0DI083YD16 5-PRIME, mRNA sequence.
ACCESSION AL554544
VERSION   AL554544.3 GI:45859296
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
REFERENCE 1 (bases 1 to 947)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE   Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On Feb 15, 2001 this sequence version replaced gi:31276354.
           Contact: Genoscope
           Genoscope - Centre National de Sequencage
           2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
           Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
           1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
           end enriched, double-strand cDNA was digested with NotI and cloned
           into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
           was normalized. Library was constructed by Life Technologies, a
           division of Invitrogen.
FEATURES   Location/Qualifiers
source   1..947
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           /mol_type="mRNA"
           /db_xref="taxon:9606"
           /clone="CS0DI083YD16"
           /tissue_type="PLACENTA COT 25-NORMALIZED"
           /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
           /note="1st strand cDNA was primed with a NotI-oligo(dT)
           primer. Five prime end enriched, double-strand cDNA was
           digested with Not I and cloned into the Not I and EcoR V
           sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match   83.8%; Score 495.8; DB 1; Length 947;
Best Local Similarity   93.2%; Pred. No. 3e-115;
Matches 521; Conservative 24; Mismatches 11; Indels 3; Gaps 3;

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Qy   36 CTGGAGTTGGTTCAGTTCAGTTCATTCTTCTTCCTCTGGCCCCTTGGGGCCCACC 95
        ||||||||||||||||| | ||| ||| || |||||||||||||||||||||||
Db  303 CTGGAGTTWGGTTMAGTTCAARTWCAARTWCATTATTCMTCTGGACCTTGGGGCCCACC 362
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(second column)

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Qy   96 TCTGAGTGAAGGGGCGTCTGCTCGCCATCACCAATGTGGAGAGGGGCGCCCCGGTGTGGG 155
        |||:|:||||||||||||||||||||||||||||||||||||||||| :|:||||||||
Db  363 TCTRARTGAAGGGGCGTCTGCMCATCACCAATGTGGAGAGGGGCGCMCMCGGTGTGGG 422

Qy  156 GTCCAGCTCTGGACACTGCTTGGCGCGGGTTCACTTTGAGTTTTCCTTTGC 215
        ||||:|:|||||||||||||||||||||||||||  ||  ||||||||| :::||
Db  423 GTCCARMTMGGACAMTGCTTGGGGCCGGGTTCACTTTGAAATATWTAAATAWWMWTTGC 482

Qy  216 TGAGCTTTTTTGGTTGTTCTTTTTATTTTTGCCTTTTATTTTTTATGAC-TATCCAGCTCTGAGA 274
        ||||||||||||||| ||| || :|||||:|||||:|||||| |:||||||
Db  483 TGAGCTTTTTTGGTTGTTGTACTTTTAWTTTTTGCATCATAWRACATATACAGCWMTGAGA 542

Qy  275 GACGGGAGTTGGAGTTGCCCGCTTACTTGGTTGGGTTGGGTTGGGGGGGCGCGGGCTGTT 334
        || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  543 GAAGGGAGTTGGAGTTGCCCGCTTACTTGGTTGGGTTGGGGGGGGCGCGGGCTGTT 602

Qy  335 TTGTTCCTTTCTTTTTAAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAG 394
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  603 TTGTTCCTTTCTTTTTTAAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAG 662

Qy  395 CTTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGTATGGGGGTGGGTTTT 454
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  663 CTTCCTCCCCACACCCCAGTA-TTGCACAATATTTGTGCGGGTATGGGGGTGGGTTTT 721

Qy  455 TAAATCTCGTTTCTCTTGACAAGCACAGGGATCCGTTCTCCTCATTTTT-GGGGTG 513
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Db  722 TAAATCTCGTTTCTCTTGACAACAGCACAGGGATCCGTTCTCCTCATTTTTTGGGGGTG 781

Qy  514 TGTGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTCTGCAGTCCCTTGCCCTGCCCGGG 573
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  782 TGTGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTCTGCAGTCCCTTGCCCGGG 841

Qy  574 CCCGTCGGGAGGCGCCATG 592
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Db  842 CCCGTCGGGAGGCGCCATG 860
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RESULT 11
BI771877
LOCUS   BI771877   932 bp   mRNA   linear   EST 25-SEP-2001
DEFINITION 603055278F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5204875 5',
           mRNA sequence.
ACCESSION BI771877
VERSION   BI771877.1 GI:15763455
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
REFERENCE 1 (bases 1 to 932)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Life Technologies, Inc.
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM11513 row: k column: 20
           High quality sequence stop: 887.
FEATURES   Location/Qualifiers
source   1..932
           /organism="Homo sapiens"
           /mol_type="mRNA"
           /db_xref="taxon:9606"
           /clone="IMAGE:5204875"
           /lab_host="DH10B"
           /clone_lib="NIH_MGC_122"
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            /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
            Site_1: NotI; Site 2: EcoRV (destroyed); RNA source
            anonymous pool of 24 week female lung, 16 week female
            spleen, and 20-22 week male spleens. Library is oligo-dT
            primed and directionally cloned (EcoRV site is destroyed
            upon cloning). Average insert size 1.4 kb, insert size
            range 1-3 kb. Library is normalized and enriched for
            full-length clones and was constructed by C. Gruber.
            (Invitrogen). Research Genetics tracking code 026. Note:
            this is a NIH_MGC Library."

ORIGIN

Query Match          81.8%;  Score 484.2; DB 3;  Length 932;
Best Local Similarity 97.6%;  Pred. No. 2.7e-112;
Matches 534;  Conservative  0;  Mismatches  8;  Indels  5;  Gaps  4;

Qy   36 CTGGAGTTGGTTCAGTTCAATTCATTCTTCCTCTGGCCCTTGGGGGCTTGGGGCCCACC 95
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  312 CTGGAGTTGGTTCAGTTCAATTCATTCTTCCTCTGGCCCTTGGGGGCTTGGGGCCCACC 371

Qy   96 TCTGAGTGAAGGGGGCGTGTCTGCCCATCACCAATGTGAGAGAGGGCGCCCCCGGTGTGGG 155
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  372 TCTGAGTGAAGGGGGCGTGTCTGCCCATCACCAATGTGAGAGAGGGCGCCCCCGGTGTGGG 431

Qy  156 GTCCAGC-TCTGGACACTGCTTGGCGGCCGGGTTCACTTGAGTTTTTCTTTG 214
          ||||||| |||||||||||||||||||||||||||||||||||||||||||
Db  432 GTCCAGCTCTGGACACTGCTTGGCGGCCGGGTTCACTTGAGTTTTTCTTTG 491

Qy  215 CTGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATTTTTGACTACTCCAGTCTGAGA 274
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  492 CTGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATTTTTGACTACTCCAGTCTGAGA 551

Qy  275 GACGGGAGTTGGAGTTGCCCGCTTTACTTGGTTGGGTTGGGTTGGGGGGGGCGGGCTGTT 334
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  552 GACGGGAGTTGGAGTTGCCCGCTTTACTTGGTTGGGTTGGGTTGGGGGGGGCGGGCTGTT 611

Qy  335 TTGTTCCTTTTCTTTTTCTTTTTTCTTTTTTAAGAGTTGGGTTTCTTTTTTTCTTTTTTAATTATCCAAACAGTGGGCAG 394
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  612 TTGTTCCTTTTCTTTTTCTTTTTTCTTTTTTAAGAGTTGGGTTTCTTTTTTTCTTTTTTAATTATCCAAACAGTGGGCAG 671

Qy  395 CTTCCTCCCCACACCCAAGTATTTGCACAATATTTGTCGGGGTATGGGGGTCGGTTTT 454
          |||||||||||| |||||||||||||||||| |||||||||| |||||||||  |||
Db  672 CTTCCTCCCCCA-ACCCAAGTATTTGCACATATTTGTCGCGGGTATGGGGGTGGG-TTC 729

Qy  455 TAAATCTCGTTTCTTGGACAAGCACAGGGATCTCGTTCGTTCCTCATTTTTGGGGGTGT 514
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Db  730 TAAATCTCGTTTCTTGGACAAGCACAGGGATCTCGTTCGTTCCTCA--TTTTGGGGGTGT 787

Qy  515 GTGGGGACTTCTCAGGTCGTGTCCCCAGCCCTTCTCTGCAGTCCCTGCCCTGGGGGC 574
          ||||||||||||||||||||||||||||||||||||||||||||||  |||  ||||
Db  788 GTGGGGACTTCTCAGGTCGTGTCCCCAGCCCTTCTCTGCAGTCCCTTCTTGCCTTGCCGGC 847

Qy  575 CCGTCGG 581
          |||||||
Db  848 CCGTCGG 854
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RESULT 12
BU145820
LOCUS   BU145820   966 bp   mRNA   linear   EST 03-SEP-2002
DEFINITION AGENCOURT_8137087 Lupski_dorsal_root_ganglion Homo sapiens cDNA
            clone IMAGE:6184135 5', mRNA sequence.
ACCESSION   BU145820
VERSION   BU145820.1 GI:22659352
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 966)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)

FEATURES   Location/Qualifiers
     source   1..966
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6184135"
                     /sex="male"
                     /tissue_type="dorsal root ganglia"
                     /dev_stage="adult, 36 yr"
                     /lab_host="DH10B"
                     /clone_lib="Lupski_dorsal_root_ganglion"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site 2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.7 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated by J. Lupski. M.D./Ph.D. (Baylor
                     College of Medicine) and is available through Life
                     Technologies."

ORIGIN

```
Query Match          80.2%;  Score 474.8; DB 5;  Length 966;
Best Local Similarity 97.4%;  Pred. No. 6.7e-110;
Matches 493;  Conservative  0;  Mismatches 12;  Indels  1;  Gaps  1;

Qy   36 CTGGAGTTGGTTCAGTTCAATTCATTCTTCCTCTGGCCCTTGGGGGCTTGGGGCCCACC 95
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Db  150 CTGGAGTTGGTTCAGTTCAATTCATTCTTCCTCTGGCCCTTGGGGGCTTGGGGCCCACC 209

Qy   96 TCTGAGTGAAGGGGGCGTGTCTGCCCATCACCAATGTGAGAGAGGGCGCCCCCGGTGTGGG 155
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Db  210 TCTGAGTGAAGGGGGCGTGTCTGCCCATCACCAATGTGAGAGAGGGCGCCCCCGGTGTGGG 269

Qy  156 GTCCAGC-TCTGGACACTGCTTGGCGGCCGGGTTCACTTGAGTTTTTCTTTG 215
          ||||||| |||||||||||||||||||||||||||||||||||||||||||
Db  270 GTCCAGCTCTGGACACTGCTTGGCGGCCGGGTTCACTTGAGTTTTTCTTTGC 329

Qy  216 TGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATTTTTGCCTCTGAGAG 275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  330 TGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATTTTTGCCTCTGAGAG 389

Qy  276 ACGGGAGTTGGAGTTGCCCGCTTTACTTGGTTGGGTTGGGTTTAATTATCCAAACAGTGGGCAGC 335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  390 ACGGGAGTTGGAGTTGCCCGCTTTACTTGGTTGGGTTGGGTTTAATTATCCAAACAGTGGGCAGC 449

Qy  336 TGTTCCTTTTCTTTTTAAGAGTTGGGTTTCTTTTCTTTTTAATTATCCAAACAGTGGGCAGC 395
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  450 TGTTCCTTTTCTTTTTAAGAGTTGGGTTTCTTTTCTTTTTAATTATCCAAACAGTGGGCAGC 509

Qy  396 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTAT-GGGGGTGGGTTTT 454
          ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db  510 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGGTGGGTTTT 569

Qy  455 TAAATCTCGTTTCTTGGACAAGCACAGGGATCTCGTTCCTCATTTTTTGGGGGTGT 514
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Db  570 TAAATCTCGTTTCTTGGACAAGCACAGGGATCTCGTTCCTCATTTTTTGGGGGCGC 629

Qy  515 GTGGGGACTTCTCAGGTCGTGTCCCC 540
          |||| |||  |||  || | |||
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Db   630 GTGGGAGACCTCCTCCGTCGCTCGAAGAACCC 655

RESULT 13
AL549255
LOCUS   AL549255   904 bp   mRNA   linear   EST 25-MAR-2004
DEFINITION AL549255 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI049YH08 5-PRIME, mRNA sequence.
ACCESSION   AL549255
VERSION   AL549255.3 GI:45749657
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 904)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE   Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On Feb 15, 2001 this sequence version replaced gi:31271075.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES   Location/Qualifiers
source   1..904
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="CS0DI049YH08"
            /tissue_type="PLACENTA COT 25-NORMALIZED"
            /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
            /note="1st strand cDNA was primed with a NotI-oligo(dT)
            primer. Five prime end enriched, double-strand cDNA was
            digested with Not I and cloned into the Not I and EcoR V
            sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match   76.6%; Score 453.6; DB 1; Length 904;
Best Local Similarity 88.4%; Pred. No. 1.7e-104;
Matches 495; Conservative 23; Mismatches 39; Indels 3; Gaps 3;

Qy   36 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGCCCCTTGGGGCTTGGGGGCCCACC 95
          |||||||||||||||||||||||||||||||:|||||||||||||||||||||:
Db   315 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGCCCCTTGGGGCTTGGGGGCCCACY 374

Qy   96 TCTGGAGTGAAGGGGGCTGTCTCGCCATCCACCAATGTGAGAGAGGCGCCCCCGGTGTGGG 155
          |||||||||||||||| |:|||| |||||||:| :|||||||||||||||||||||||||
Db   375 TCTGGAGTGAAGGGGGCTGTGTTCGCCCWTCCACCAWGTGGNAAAGGCGCCCCCGGTGTGGG 434

Qy   156 GTTCCAGCTCTGGACACTGCTTGGCCGGCCGGGGTTCACTTGAGTTTTCTTTGC 215
          ||||||||||||||| ||||| | ||:|||||||||||||||||||||||||
Db   435 GTTCCAGCTCTGGACACTGCTTGGCCGGCCGGGGTTCACTTWGAGTTTTCTTTGC 494

Qy   216 TGAGCTTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG 275
          |||||||||||||| |||||::|||| :|:||| : :|:   : ||
Db   495 TGAGCTTTTTTGGTTGTTCYTTTAWTTTTTGCSCSYTTAWGGAAYAAGCCAMYACGCRAA 554

Qy   276 ACGGGAGTTGGAGTTGCCCGCTTACTTTGGTTGGGGTGGGGGGCCGGCGGGGCTGTTT 335
          || | | ||||||||||||||||||||: |||||||||||||:||||||||:||||||
Db   555 AAGGGCGTTTGGGGTTGACCCACTTWATTTGGTTGGTTGGTTGGGGGGGNSGCSGGCTGTTT 614

Qy   336 TGTTCC--TTTTCTTTTTTAAGAGTGGGTTTTCTTTTTAATTATCCAACAGT-GGGCA 393
          |||| :|| | :||||||||| | | | ||||||:||||||||||||:||| :|||
Db   615 TGTTYCTTTTCTTTTTTTAAAWTGGGTTTTCTTTTTWAATAWCCAAMAATGGGGCC 674

Qy   394 GCTTCCTCCCCCACACCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGGTGTGGG 453
          :||| | :| |||||||||| | || ||||| ||||||||||| |||||||:||||||

RESULT 14
BI770311
LOCUS   BI770311   940 bp   mRNA   linear   EST 25-SEP-2001
DEFINITION 603056215F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5205698 5',
            mRNA sequence.
ACCESSION   BI770311
VERSION   BI770311.1 GI:15761889
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 940)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D:
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM1515 row: n column: 03
            High quality sequence stop: 862.
FEATURES   Location/Qualifiers
source   1..940
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:5205698"
            /lab_host="DH10B"
            /clone_lib="NIH_MGC 122"
            /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
            Site 1: NotI, Site 2: EcoRV (destroyed); RNA source
            anonymous pool of 24 week female lung, 16 week female
            spleen, and 20-22 week male spleens. Library is oligo-dT
            primed and directionally cloned (EcoRV site is destroyed
            upon cloning). Average insert size 1.4 kb, insert size
            range 1-3 kb. Library is normalized and enriched for
            full-length clones and was constructed by C. Gruber
            (Invitrogen). Research Genetics tracking code 026. Note:
            this is a NIH_MGC Library."
ORIGIN

Query Match   76.6%; Score 453.4; DB 3; Length 940;
Best Local Similarity 94.3%; Pred. No. 1.9e-104;
Matches 525; Conservative 0; Mismatches 26; Indels 6; Gaps 5;

Qy   36 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGCCCCTTGGGGCTTGGGGGCCCACC 95
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   327 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGCCCCTTGGGGCTTGGGGGCCCACC 386

Qy   96 TCTGAGTGAAGGGGGCTGTCTCGCCATCCACCAATGTGAGAGAGGGCGCCCCCGGTGTGGG 155

Db   675 RCTTCCTCCCCCACACCAAATATTTGCAAAATATTTGTGCGGGGTATGGGGGTGGGGTTT 734

Qy   454 TTAAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCCTTCCTCATTTT-GGGGT 512
          |||||||||||||||||||||||||||||||||||||||||||||||||| : ||||
Db   735 TTAAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCCTTCCTCATTTTTKGGGGT 794

Qy   513 GTGTGGGGACTTCTCAGTGCGTGTCCCAGCCTTCTGCAGTCCCTTCTGCCCTGCCGG 572
          ||||||||||||||||||||||||||||||||||||||:|||:||:||||||||||||
Db   795 GTGTGGGGACTTCTCAGTGCGTGTCCCAGCCCTTCTGCAGTYCCTTCTGCCCTGCCGG 854

Qy   573 GCCCGTCGGGAGGCGCCATG 592
          ||||||||||||||||||||
Db   855 GCCCGTCGGGAGGCGCCATG 874

pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male.. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN

```
Query Match      76.1%;   Score 450.8;  DB 3;  Length 861;
Best Local Similarity  96.1%;  Pred. No. 8.6e-104;
Matches 537;  Conservative   0;  Mismatches  13;  Indels   9;  Gaps   7;

Qy     36 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGGGCCTTGGGGCCCACC   95
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    247 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGGCCCTTGGGGCCCACC  306

Qy     96 TCTGAGTGAAGGGGGCGTGCTGCCATCACCAATGTGGAGAGGGCGCCCCGGTGTGGG  155
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    307 TCTGAGTGAAGGGGGCGTGCGCCCCATCACCAACCAATGTGGAGAGGGCGCCCCGGTGTGGG  366

Qy    156 GTCCAGCTCTGGACACTGCTTGGCGCGCCGGGTTCACTTGAGTTTTTCTTTGC  215
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    367 GTCCAGCTCTGGACACTGCTTGGGCG-CGGGTTCACTTGAGTTTTTAAGTTTTTCTTTGC  425

Qy    216 TGAGCTTTTTTGGTTGTTCTTTTATTTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG  275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    276 ACGGGAGTTTGGAGTTGCCGCCTTTACTTTGGTTGGGTTGGGGGGCGGCGGGGCTGTTT  335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    567 ACGGGAGTTTGGAGTTGCCCCGCTTTACTTTTGGTTGGGTTGGGGGGGCGGCGGGGCTGTTT  626

Qy    216 TGTTCCTTTTTCTTTTTTAAGAGTTGGGTTTTCTTTTTTTTAATTATCCAAACAGTGGGCAGC  275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    426 TGAGCTTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG  485

Qy    276 ACGGGAGTTTGGAGTTGCCCGCTTTACTTGGTTGGGTTGGGTTGGGGGGGCGGGGCTGTTT  335
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Db    486 ACGGGAGTTTGGAGTTGCCCGCTTTACTTGGTTGGGTTGGGTTGGGGGGGCGGGGCTGTTT  545

Qy    336 TGTTCCTTTTTCTTTTTTAAGAGTTGGGTTTTCTTTTTTTTAATTATCCAAACAGTGGGCAGC  395
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Db    546 TGTTCCTTTTTCTTTTTTAAGAGTTGGGTTTTCTTTTTTTTAATTATCCAAACAGTGGGCAGC  605

Qy    396 TTCCTCCCCACACCCAAGTATTTGCACAATATTGTGCGGGTATGGGGGTGGGTTTT  455
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Qy    456 AAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCGTTCTTCCTCGTCCGTCCTCTCGCCG  514
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    664 AAATCTCG-TTCTCTTGGACAACAGCACAGGGATCTCGTTCGTTCTTCCTCATTTTTTGGCGGTGT  722

Qy    515 GTGGGGACTTCTCAGTTCGTG---TCCCCAGCCTTCTCTCGCAGTCCCTTCTGCCCG  571
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Db    723 GTGGGGACTTCTCCAGGGTCGTGTTCCCCAGCTTCTCTTGCAGTCCCTTCTGCCCG  782

Qy    572 GGCCCGTCGGGAGGGCCCA  590
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Db    783 GG-CCGTCGGGAGGGCGCCA  800
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Search completed: April 3, 2006, 06:38:18
Job time : 3498 secs

Db   387 TCTGAGTGAAGGGGGCGTGCTGCCATCACCAATGTGGAGAGGGCGCCCCGGTGTGGG 446
Qy   156 GTCCAGCTCGGACACTGCTTGGGCGCGGGTTCACTTGAGTTTTTCTTTGC 215
Db   447 GTCCAGCTCTGGACACTGCTTGGGCGCGGGTTCACTTTGAGTTTTTCTTTGC 506
Qy   216 TGAGCTTTTTTGGTGTTCTTTTATTTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG 275
Db   507 TGAGCTTTTTTGGTGTTCTTTTATTTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG 566
Qy   276 ACGGGAGTTGGAGTTGCCGCCTTTACTTTGGTTGGGTTGGGGGGCGGCGGGGGCTGTTT 335
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Qy   336 TGTTCCTTTTTCTTTTTTTAAGAGTGGGTTTTCTTTTTTTTAATTATCCAAACAGTGGGCAGC 395
Db   627 TGTTCCTTTTTCTTTTTTTAAGAGTTGGG--TTTTCTTTTTTTAATTATCCAAACAGTGGGCAGC 685
Qy   396 TTCCTCCCCACACCCAAGTATTTGTGCGGGTATATTGTGCGGGTATGGGGGGTGTTTTT 455
Db   686 TTCCTCCCCCA-ACCCAAGTATTTGTGCACAATATTGTGCGGGGTATGGGCGGTGGGGTT 744
Qy   456 AAATCTCGTTTCTCTGGACAAGCACAGGGATCTCGTTCGTTCTTCCTCATTTTTTTGGGGTGTG 515
Db   745 AAATCTCGTTTCTCTGGACAGGGACACA-GGATCTCGTTCTGTTCCTCA-TTTAAGGGGGTGTG 802
Qy   516 TGGGGACTTCTCAGTCGTGTCCCCAGCCCTTCTCTCGCAGTCCCTGCCGGCC 575
Db   803 TGGGGACTTCTCAGTTCCGTCGTCCCCAGCTTATCTGAAGTCC--TTCTGCCTGCGGGGCC 860
Qy   576 CGTCGGGAGGCGCCATG 592
Db   861 CGTCGGGAGGGCCCATG 877

RESULT 15
BI834269
LOCUS   BI834269   861 bp   mRNA   linear   EST 04-OCT-2001
DEFINITION 603084178F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5223331 5',
            mRNA sequence.
ACCESSION   BI834269
VERSION   BI834269.1 GI:15945819
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 861)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/,
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11561 row: 1 column: 20
            High quality sequence stop: 830.
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
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                     /clone="IMAGE:5223331"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_120"
                     /note="Organ: pooled pancreas and spleen; Vector:

GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2006, 05:39:30 ; Search time 467 Seconds
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                                     8448.604 Million cell updates/sec

Title: US-10-624-670-1
Perfect score: 592
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Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 496997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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            12: geneseqn2004as:*
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            14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	592	100.0	592	12	ADJ57079	Adj57079 Metastati
2	557	94.1	1692	10	ADC99124	Adc99124 Human KPP
3	557	94.1	2181	12	ADQ22123	Adq22123 Human sof
4	557	94.1	2850	6	ABL92112	Abl92112 Human Tum
5	557	94.1	2850	10	ABX72037	Abx72037 DNA encod
6	555	93.8	909	12	ADI28112	Adi28112 Human PRL
7	551	93.1	986	12	ADJ57080	Adj57080 Metastati
8	410.6	69.4	1859	10	ADC99125	Adc99125 Human KPP
9	337	56.9	1320	11	ADN95384	Adn95384 Human BEC
10	337	56.9	1321	12	ADI28097	Adi28097 Human pro
11	337	56.9	1321	12	ADI57209	Adi57209 Human PRL
12	337	56.9	1321	12	ADP21390	Adp21390 Gene PTP4
13	337	56.9	1396	12	ADI28111	Adi28111 Human sig
14	337	56.9	1396	12	ADN75973	Adn75973 Human sig
15	337	56.9	1396	12	ADP20802	Adp20802 Human pro
16	334	56.4	334	13	ADR12326	Adr12326 Human pro
17	310	52.4	982	10	ACA56395	Aca56395 Human sig
18	310	52.4	982	12	ADI56191	Adi56191 Human.pol
19	310	52.4	984	2	AAV29127	Aav29127 HPTP-2 co
20	274.4	46.4	671	12	ADI28113	Adi28113 Human PRL
21	240	40.5	462	12	ADQ17386	Adq17386 Human sof
22	240	40.5	1006	12	ADI28332	Adi28332 Human pro
23	240	40.5	1006	14	AEA36203	Aea36203 Human nuc
24	236.4	39.9	358	3	AAA43595	Aaa43595 Human sec
25	234	39.5	1315	3	AAA09025	Aaa09025 Human CSA
26	221	37.3	773	12	ADO26263	Ado26263 C35 promo
27	139	23.5	1678	12	ADI28192	Adi28192 Mouse cDN
28	131.4	22.2	3222	12	ADI28104	Adi28104 Mouse cDN
29	64	10.8	527	14	ACL56361	Acl56361 Human col
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32 c	52.8	8.9	1260	6	ABQ16903	Abq16903 Oligonucl
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34	52	8.8	7758	6	ABL33103	Abl33103 Human imm
35 c	51.2	8.6	192	13	ACN50408	Acn50408 Cotton ma
36	51	8.6	629	10	ABT21705	Abt21705 Breast ca
37	50.8	8.6	7698	6	ABL33700	Abl33700 Human imm
38 c	50.4	8.5	1025	6	ABQ25831	Abq25831 Oligonucl
39	50.4	8.5	1025	6	ABQ25830	Abq25830 Oligonucl
40	49.2	8.3	509	6	ABQ18800	Abq18800 Oligonucl
41 c	49.2	8.3	509	6	ABQ18801	Abq18801 Oligonucl
42	48.8	8.2	7721	14	AEA18095	Aea18095 Converted
43	48.6	8.2	565	6	ABQ17072	Abq17072 Oligonucl
44 c	48.6	8.2	565	6	ABQ17073	Abq17073 Oligonucl
45	48.6	8.2	5203	10	ADB54278	Adb54278 Pretreat

ALIGNMENTS

RESULT 1
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ID   ADJ57079 standard; DNA; 592 BP.
XX
AC   ADJ57079;
XX
DT   06-MAY-2004 (first entry)
XX
DE   Metastatic colon cancer-specific transcriptional regulatory element.
XX
KW   Human; PRL-3; promoter; transcriptional regulatory element; gene therapy;
KW   colon cancer; metastasis; cytostatic; gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200400790-A2.
XX
PD   29-JAN-2004.
XX
PF   22-JUL-2003; 2003WO-US023032.
XX
PR   22-JUL-2002; 2002US-0397859P.
XX
PA   (CELL-) CELL GENESYS INC.
XX
PI   Li Y; Yu DC;
XX
DR   WPI; 2004-123388/12.
XX
PT   New colon cancer transcriptional regulatory element (TRE) sequence that
PT   is specific for metastatic colon cancer cells, useful as a promoter for
PT   specific virus replication.
XX
PS   Claim 4; SEQ ID NO 1; 39pp; English.
XX
CC   The present sequence is that of a colon cancer transcriptional regulatory
CC   element (TRE) derived from the human PRL-3 gene in the region upstream of
CC   the translational start codon. The PRL-3 protein tyrosine phosphatase
CC   gene is specifically expressed at a high level in metastatic colon
CC   cancers. The invention provides replication-competent adenoviral vectors
CC   comprising the present sequence operably linked to a gene required for
CC   virus replication. Methods are provided for introducing into a cell an

CC   adenoviral vector comprising a metastatic colon cancer-specific TRE
CC   operably linked to a gene required for virus replication, and host cells
CC   comprising the adenovirus vector. Methods are also provided for
CC   conferring selective cytotoxicity in target colon cancer cells,
CC   particularly metastatic colon cancer cells, by contacting the cells with
CC   an adenovirus vector of the invention, where the vector enters the cell
CC   and propagates virus. By providing for transcriptional initiating
CC   regulation dependent upon transcription factors that are only active in
CC   specific, limited cell types, virus replication is restricted to target
CC   cells.
XX
SQ   Sequence 592 BP; 75 A; 141 C; 178 G; 198 T; 0 U; 0 Other;

Query Match   100.0%;   Score 592;   DB 12; Length 592;
Best Local Similarity 100.0%;   Pred. No. 1.8e-142;
Matches 592; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CTATAGGGCACGCGTCGGTCGACGGCCCGGGCTGGTCGAGTTGGTTCAGTTCAAGTTCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CTATAGGGCACGCGTCGGTCGACGGCCCGGGCTGGTCGAGTTGGTTCAGTTCAAGTTCA 60

Qy   61 TTCTTCCTCTGGCCCTTGGGGGCTTGGGGCCCACCTCTGAGTGAAGGGGGCTGTCTGCCC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TTCTTCCTCTGGCCCTTGGGGGCTTGGGGCCCACCTCTGAGTGAAGGGGGCTGTCTGCCC 120

Qy   121 ATCCACCAATGTGGAGAGGGCGCCCCGGTGTGGGGTCCAGCTCTGGACACTGCTTGGCG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ATCCACCAATGTGGAGAGGGCGCCCCGGTGTGGGGTCCAGCTCTGGACACTGCTTGGCG 180

Qy   181 GCCGGGTCACTTGAGTTTTCTTGCTGAGCTTTTTTGGTTGTTCTTTTTA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GCCGGGTCACTTGAGTTTTCTTGCTGAGCTTTTTTGGTTGTTCTTTTTA 240

Qy   241 TTTTTTGCCCTTTATGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGCCCGCTTT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TTTTTTGCCCTTTATGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGCCCGCTTT 300

Qy   301 ACTTTGGGTTGGGTTGGGGGGGGCGGCGGCGGGGCGTGTTTGTTCCTTTTCTTTTTTAAGAGTTG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 ACTTTGGGTTGGGTTGGGGGGGGCGGCGGCGGGGCGTGTTTGTTCCTTTTCTTTTTTAAGAGTTG 360

Qy   361 GGTTTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCCCCCCACACCCAAGTATTTG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GGTTTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCCCCCCACACCCAAGTATTTG 420

Qy   421 CACAATATTTGTGCGGGGTATGGGGGTGGGTTTTTAAATCTCGTTCTTCTTTGGACAAGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CACAATATTTGTGCGGGGTATGGGGGTGGGTTTTTAAATCTCGTTCTTCTTTGGACAAGCA 480

Qy   481 CAGGGATCTCGTTCCTCCATTTTTGGGGGTGTGGGGACTTCCAGTCGTGTCCCC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CAGGGATCTCGTTCCTCCATTTTTGGGGGTGTGGGGACTTCCAGTCGTGTCCCC 540

Qy   541 AGCCTTCCTGCAGTCCCCTTCTGCCCCTGCCCCTGCCGGGCCGTCGGGAGGCGCCATG 592
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AGCCTTCCTGCAGTCCCCTTCTGCCCCTGCCCCTGCCGGGCCGTCGGGAGGCGCCATG 592

RESULT 2
ADC99124
ID   ADC99124 standard; cDNA; 1692 BP.
XX
AC   ADC99124;
XX
DT   01-JAN-2004 (first entry)
XX
DE   Human KPP cDNA - SEQ ID 77.
XX
KW   anti-HIV; antiallergic; antiinflammatory; antianaemic; antiparkinsonian;
KW   nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;
KW   immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;
KW   antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective;
KW   osteopathic; antiarthritic; antiparasitic; antihelminthic; antipsoriatic;

KW   uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;
KW   virucide; protozoacide; fungicide; fungistatic; kinase; phosphatase; KPP;
KW   cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;
KW   cancer; developmental; mental retardation; neurological;
KW   Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;
KW   diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;
KW   helminthic infection; transgenic; gene therapy; human; ss; gene.
XX
OS   Homo sapiens.
XX
PN   WO200303680-A2.
XX
PD   24-APR-2003.
XX
PF   17-OCT-2002; 2002WO-US033723.
XX
PR   19-OCT-2001; 2001US-0345474P.
PR   02-NOV-2001; 2001US-0343910P.
PR   13-NOV-2001; 2001US-0333098P.
PR   16-NOV-2001; 2001US-0332424P.
PR   30-NOV-2001; 2001US-0334288P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;
PI   Emerling BM, Forsythe IJ, Gandhi AR, Gorvad AE, Griffin JA;
PI   Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lee SY;
PI   Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;
PI   Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;
PI   Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;
PI   Zebarjadian Y;.
XX
DR   WPI; 2003-403214/38.
DR   P-PSDB; ADC99072.
XX
PT   New human kinases and phosphatases and polynucleotides, useful for
PT   diagnosing, treating or preventing autoimmune or inflammatory disorders
PT   (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
PT   cancer or hepatitis.
XX
PS   Claim 5; SEQ ID NO 77; 424pp; English.
XX
CC   The invention relates to a novel isolated polypeptide which is a human
CC   kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,
CC   agonists and antagonists are useful for diagnosing, treating or
CC   preventing cell proliferative disorders such as atherosclerosis,
CC   cirrhosis, hepatitis and cancer, developmental disorders e.g. mental
CC   retardation, neurological disorders including Alzheimer's disease and
CC   Parkinson's disease, autoimmune and inflammatory disorders such as
CC   Crohn's disease and diabetes mellitus and finally, viral, bacterial,
CC   fungal, parasitic, protozoan or helminthic infections. Furthermore, the
CC   polynucleotides encoding KPP may be useful for creating transgenic
CC   animals to model human disease, as well as during gene therapy
CC   procedures. The current sequence is that of the human KPP cDNA of the
CC   invention.
XX
SQ   Sequence 1692 BP; 268 A; 485 C; 535 G; 404 T; 0 U; 0 Other;

Query Match   94.1%;   Score 557; DB 10; Length 1692;
Best Local Similarity 100.0%; Pred. No. 2.6e-133;
Matches 557; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   36 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGGCCCTTGGGGGCTTGGGGCCCACC 95
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   480 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGGCCCTTGGGGGCTTGGGGCCCACC 539

Qy   96 TCTGAGTGAAGGGGGCTGTCTGCCCATCCACCAATCGTGCCCATCCACCAATGTGGAGAGGGCGCCCCCGGTGTGGG 155
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   540 TCTGAGTGAAGGGGGCTGTCTGCCCATCCACCAATCGTGCCCATCCACCAATGTGGAGAGGGCGCCCCCGGTGTGGG 599

Qy   156 GTCCAGCTCTGGACACTGCTTGGCGGCCGGGTCACTTGAGTTTTCTTGC 215
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   600 GTCCAGCTCTGGACACTGCTTGGCGGCCGGGTCACTTGAGTTTTCTTGC 659

```
Qy  216 TGAGCTTTTTTGGTGTGTTCTTTTTATTTTTTGGCCTCTTTATGACTATCCAGCTCTGAGAG 275
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  660 TGAGCTTTTTTGGTGTGTTCTTTTTATTTTTTGGCCTCTTTATGACTATCCAGCTCTGAGAG 719

Qy  276 ACGGGAGTTGGAGTTGCCCGCTTACTTGGTTGGTTTGGGTTGGGGGGGCGGGGGCTGTTT 335
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  720 ACGGGAGTTGGAGTTGCCCGCTTACTTGGTTGGTTTGGGTTGGGGGGGCGGGGGCTGTTT 779

Qy  336 TGTTCCTTTCTTTTCTTTTTTAAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGGCAGC 395
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  780 TGTTCCTTTCTTTTCTTTTTTAAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGGCAGC 839

Qy  396 TTCCTCCCCACACCCAAGTATTGCACAATATTTGTGCGGGGTATGGGGGTGGGTTTTT 455
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  840 TTCCTCCCCACACCCAAGTATTGCACAATATTTGTGCGGGGTATGGGGGTGGGTTTTT 899

Qy  456 AAATCTCGTTTCTTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTGGGGGTG 515
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  900 AAATCTCGTTTCTTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTGGGGGTG 959

Qy  516 TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTCGCAGTCCCTTCTGCCCTGCCGGCC 575
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  960 TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTCGCAGTCCCTTCTGCCCTGCCGGCC 1019

Qy  576 CGTCGGGAGGGCGCCATG 592
        ||||||||||||||||||
Db 1020 CGTCGGGAGGGCGCCATG 1036
```

RESULT 3
ADQ22123
ID ADQ22123 standard; DNA; 2181 BP.
XX
AC ADQ22123;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4943.
XX
KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
KW ds.
XX
OS Homo sapiens.
XX
PN WO200048938-A2.
XX
PR 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US038193.
XX
PR 26-NOV-2002; 2002US-0429739P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Aziz N, Ginsburg WM, Zlotnik A;
XX
DR WPI; 2004-441208/41.
XX
PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
PS Example 2; SEQ ID NO 4943; 210pp; English.
XX
CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has

CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
XX specification per se but was submitted in CD format by the inventor.
SQ Sequence 2181 BP; 512 A; 649 C; 546 G; 474 T; 0 U; 0 Other;

Query Match   94.1%; Score 557; DB 12; Length 2181;
Best Local Similarity   100.0%; Pred. No. 2.8e-133;
Matches 557; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy  36 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGCGGCCCTTGGGGGCTTGGGGGCCACC 95
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 316 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGCGGCCCTTGGGGGCTTGGGGGCCACC 375

Qy  96 TCTGAGTGAAGGGGGCTGTCGCCATCCACCAATGTGGAGAGGGGCGCCCCCGTGTGGG 155
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 376 TCTGAGTGAAGGGGGCTGTCGCCATCCACCAATGTGGAGAGGGGCGCCCCCGTGTGGG 435

Qy 156 GTCCAGCTCTGGACACTGCTTGGCGGCCGGGTTCACTTTGAGTTTTCTTGC 215
       |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 436 GTCCAGCTCTGGACACTGCTTGGCGGCCGGGTTCACTTTGAGTTTTCTTGC 495

Qy 216 TGAGCTTTTTTGGTGTGTTCTTTTTATTTTTTGGCCTCTTTATGACTATCCAGCTCTGAGAG 275
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 496 TGAGCTTTTTTGGTGTGTTCTTTTTATTTTTTGGCCTCTTTATGACTATCCAGCTCTGAGAG 555

Qy 276 ACGGGAGTTGGAGTTGCCCGCTTACTTGGTTGGGTTTCTTTTTAATTATCCAAACAGTGGCAGC 335
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 556 ACGGGAGTTGGAGTTGCCCGCTTACTTGGTTGGGTTTCTTTTTAATTATCCAAACAGTGGCAGC 615

Qy 336 TGTTCCTTTCTTTCTTTTTTAAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGGCAGC 395
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 616 TGTTCCTTTCTTTCTTTTTTAAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGGCAGC 675

Qy 396 TTCCTCCCCACACCCAAGTATTGCACAATATTTGTGCGGGGTATGGGGGTGGGTTTT 455
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 676 TTCCTCCCCACACCCAAGTATTGCACAATATTTGTGCGGGGTATGGGGGTGGGTTTT 735

Qy 456 AAATCTCGTTTCTTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTGGGGGTG 515
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 736 AAATCTCGTTTCTTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTGGGGGTG 795

Qy 516 TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCCTTCTGCGAGTCCCTGCCGGCC 575
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 796 TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCCTTCTGCGAGTCCCTGCCGGCC 855

Qy 576 CGTCGGGAGGGCGCCATG 592
       ||||||||||||||||||
Db 856 CGTCGGGAGGGCGCCATG 872
```

RESULT 4
ABL92112
ID ABL92112 standard; cDNA; 2850 BP.
XX
AC ABL92112;
XX
DT 30-MAY-2002 (first entry)
XX
DE Human Tumour Endothelial Marker polynucleotide SEQ ID NO 247.
XX
KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
KW normal endothelial marker; pan-endothelial marker; immunostimulant;
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
KW psoriasis; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200210217-A2.

```
Qy  516  TGGGGACTTCTCAGTCGTGTCCCAGCGCCTTCTGCGCCTTCTGCGCCTGCCCGGGGCC  575
         ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db  825  TGGGGACTTCTCAGTCGTGTCCCCAGCGCCTTCTGCGCCTTCTGCGCCTGCCCGGGGCC  884

Qy  576  CGTCGGGAGGCGCCATG  592
         |||||||||||||||||
Db  885  CGTCGGGAGGCGCCATG  901
```

RESULT 5
ABX72037
ID   ABX72037 standard; DNA; 2850 BP.
XX
AC   ABX72037;
XX
DT   12-MAR-2003 (first entry)
XX
DE   DNA encoding human tumour endothelial marker TEM 29.
XX
KW   Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
KW   Tumour endothelial marker; normal endothelial marker; PEM;
KW   pan-endothelial marker; polycystic kidney disease; psoriasis;
KW   diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
KW   neoangiogenesis; immune response; cytostatic; antidiabetic; gene;
KW   ophthalmological; antirheumatic; antiarthritic; antipsoriatic; ds.
XX
OS   Homo sapiens.
XX
PN   WO200283874-A2.
XX
PD   24-OCT-2002.
XX
PF   10-APR-2002; 2002WO-US008253.
XX
PR   11-APR-2001; 2001US-0282850P.
PR   06-FEB-2002; 2002US-0354262P.
XX
PA   (UVJO) UNIV JOHNS HOPKINS.
XX
PI   Carson-Walter B, St Croix B, Kinzler KW, Vogelstein B;
XX
DR   WPI; 2003-093016/08.
DR   P-PSDB; ABU54465.
XX
PT   New purified human transmembrane protein, designated as tumor endothelial
PT   marker (TEM) 3, useful for detecting, diagnosing or treating tumors,
PT   polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
PT   psoriasis.
XX
PS   Disclosure; Page 263-264; 374pp; English.
XX
CC   The present invention relates to a novel method for the isolation of
CC   endothelial cells (ECs), and the identification of genes expressed in
CC   normal and tumour ECs. Tumour endothelial marker (TEM), normal
CC   endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
CC   identified in human ECs. The human EC marker proteins and the
CC   polynucleotide sequences encoding them are useful for detecting,
CC   diagnosing or treating tumours as well as polycystic kidney disease,
CC   diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also
CC   useful for inhibiting neoangiogenesis or tumour angiogenesis, for
CC   inducing an immune response to tumour endothelial cells in a patient, or
CC   for identifying candidate drugs for treating tumours. The present
CC   sequence represents a human TEM or NEM gene of the invention
XX
SQ   Sequence 2850 BP; 452 A; 863 C; 916 G; 619 T; 0 U; 0 Other;

Query Match   94.1%; Score 557; DB 10; Length 2850;
Best Local Similarity   100.0%; Pred. No. 3e-133;
Matches 557; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy   36  CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGGCCCTTGGGGGCTTGGGGCCCACC   95
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   36  CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGGCCCTTGGGGGCTTGGGGCCCACC   95
```

XX
PD   07-FEB-2002.
XX
PF   01-AUG-2001; 2001WO-US024031.
XX
PR   02-AUG-2000; 2000US-0222599P.
PR   11-AUG-2000; 2000US-0224360P.
PR   11-APR-2001; 2001US-0282850P.
XX
PA   (UVJO) UNIV JOHNS HOPKINS.
XX
PI   St Croix B, Kinzler KW, Vogelstein B;
XX
DR   WPI; 2002-291856/33.
DR   P-PSDB; ABB90758.
XX
PT   An isolated molecule comprising an antibody variable region which
PT   specifically binds to an extracellular domain of a tumor endothelial
PT   marker (TEM) protein, useful for inhibiting tumor growth.
XX
PS   Claim 65; Page 240; 331pp; English.
XX
CC   The invention relates to an isolated molecule comprising an antibody
CC   variable region which specifically binds to an extracellular domain of a
CC   tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
CC   ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
CC   proteins have cytostatic, immunostimulant and antiangiogenic activity.
CC   They are useful for inhibiting tumour growth, neoangiogenesis in subjects
CC   bearing a vascularised tumour, polycystic kidney disease, diabetic
CC   retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
CC   genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
CC   are disclosed, as are marker oligonucleotide sequences: tumour
CC   endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
CC   endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
CC   (PEM) ABL91903-ABL91995
XX
SQ   Sequence 2850 BP; 452 A; 863 C; 916 G; 619 T; 0 U; 0 Other;

Query Match   94.1%; Score 557; DB 6; Length 2850;
Best Local Similarity   100.0%; Pred. No. 3e-133;
Matches 557; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy   36  CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGGCCCTTGGGGGCTTGGGGCCCACC   95
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  345  CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGGCCCTTGGGGGCTTGGGGCCCACC  404

Qy   96  TCTGAGTGAAGGGGGCTGTCTGCCCATCCACCAATGTGGAGAGGGCGCCCCCGTGTGGG  155
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  405  TCTGAGTGAAGGGGGCTGTCTGCCCATCCACCAATGTGGAGAGGGCGCCCCCGTGTGGG  464

Qy  156  GTCCAGCTCTGGACACTGCTTGGGCGGGCCGGGTTCACTTTGAGTTTTAAGTTTTCTTTGC  215
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  465  GTCCAGCTCTGGACACTGCTTGGGCGGGCCGGGTTCACTTTGAGTTTTAAGTTTTCTTTGC  524

Qy  216  TGAGCTTTTTGGTTGTTCTTTTATTTTGCCCTTTATGACTATCCAGCTCTGAGAG  275
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  525  TGAGCTTTTTGGTTGTTCTTTTATTTTGCCCTTTATGACTATCCAGCTCTGAGAG  584

Qy  276  ACGGGAGTTTGGAGTTGCCCGCTTTACTTTGGTTGGGTGGGGGGCGGCGGCCTGTTT  335
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  585  ACGGGAGTTTGGAGTTGCCCGCTTTACTTTGGTTGGGTGGGGGGCGGCGGCCTGTTT  644

Qy  336  TGTTCCTTTTCTTTTAAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGC  395
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  645  TGTTCCTTTTCTTTTAAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGC  704

Qy  396  TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGGTGGGTTTTT  455
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  705  TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGGTGGGTTTTT  764

Qy  456  AAATCTCGTTTCTTGGACAAGCACAGGGATCTCGTTTCCCTCATTTTTTGGGGGTGTG  515
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  765  AAATCTCGTTTCTTGGACAAGCACAGGGATCTCGTTTCCCTCATTTTTTGGGGGTGTG  824
```

PT
XX
PS   Example 15; SEQ ID NO 19; 77pp; English.
XX
CC
CC   The invention relates to a compound comprising a sequence comprising 8-80
CC   base pairs (bp) targeted to a nucleic acid encoding protein tyrosine
CC   phosphatase type IVA member 3 (PRL-3), that specifically hybridises with
CC   the nucleic acid encoding PRL-3 and inhibits expression of PRL-3, i.e. is
CC   an antisense oligonucleotide (AO). Also included are a composition
CC   comprising the compound and a carrier or diluent, inhibiting the
CC   expression of PRL-3 in cells or tissues, treating an animal having or
CC   suspected of having a disease or condition associated with PRL-3 and
CC   screening for an antisense compound. The antisense oligonucleotide is
CC   useful for preparing a composition for treating hyperproliferative
CC   disorder, particularly cancer ((e.g. colorectal cancer), diabetes,
CC   reduced glucose tolerance, insulin resistance and obesity. The present
CC   sequence is a Human PRL3 target cDNA sequence.
XX
SQ   Sequence 909 BP; 120 A; 273 C; 271 G; 242 T; 0 U; 3 Other;

```
Query Match             93.8%;  Score 555;  DB 12;  Length 909;
Best Local Similarity   99.6%;  Pred. No. 6.9e-133;
Matches  555;  Conservative   1;  Mismatches   1;  Indels   0;  Gaps   0;

Qy     36 CTGGAGTTGGTTCAGTTCAAGTTCATTCTCCTGCCCTTGGGGGCTTGGGCCCACC 95
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    317 CTGGAGTTGGTTCAGTTCAAGTTCATTCTCCTGCCCTTGGGGGCTTGGGCCCACC 376

Qy     96 TCTGAGTGAAGGGGGCTGTGTCTGCCCATCCACCAATGTGGAGAGGGCGCCCCGGTGTGGG 155
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    377 TCTGAGTGAAGGGGGCTGTGTCTGCCCATCCACCAATGTGGAGAGGGCGCCCCGGTGTGGG 436

Qy    156 GTCCAGCTCTGGACACTGCTTGCGGCGGTCTGGCGGGCGCGGGCGCCCCGGTGTTTCTTGC 215
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    437 GTCCAGCTCTGGACACTGCTTGCGGCGGTCTGGCGGGCGCGGGCGCCCCGGTGTTTCTTGC 496

Qy    216 TGAGCTTTTTTGGTGTGTTCTTTTTATTTTTATTTTTTATGACTATCCAGCTCTGAGAG 275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    497 TGAGCTTTTTTGGTGTGTTCTTTTTATTTTTATTTTTTATGACTATCCAGCTCTGAGAG 556

Qy    276 ACGGGAGTTTGGAGTTGGAGTTGCCCGCTTTACTTTGGGGGGGTATGGGGGTGGGTGTTT 335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    557 ACGGGAGTTTGGAGTTGGAGTTGCCCGCTTTACTTTGGGGGGGTATGGGGGTGGGTGTTT 616

Qy    336 TGTTCCTTTTCTTTTTTTAAGAGTTGGGTTTTCTTTTTTTAATTATCCAAACAGTGGGCAGC 395
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    617 TGTTCCTTTTCTTTTTTTAAGAGTTGGGTTTTCTTTTTTTAATTATCCAAACAGTGGGCAGC 676

Qy    396 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGGTGGGTTTTT 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    677 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGGTGGGTTTTT 736

Qy    456 AAATCTCGTTTCTTCTTGGACAAGCACAGGGATCTCGTTCGTTCTCCTCATTTTTGGGGGTG 515
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    737 AAATCTCGTTTCTTCTTGGACAAGCACAGGGATCTCGTTCGTTCTCCTCATTTTTGGGGGTG 796

Qy    516 TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCCCTTCCAGTCCCTTCGCCTGCCGGGCC 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    797 TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCCCTTCCAGTCCCTTCGCCTGCCGGGCC 856

Qy    576 CGTCGGGAGGCGCCATG 592
          |||||||||||||||||
Db    857 CGTCGGGAGGCGCCATG 873
```

RESULT 7
ADJ57080
ID   ADJ57080 standard; DNA; 986 BP.
XX
AC   ADJ57080;
XX
DT   06-MAY-2004 (first entry)
XX

RESULT 6
ADI28112
ID   ADI28112 standard; cDNA; 909 BP.
XX
AC   ADI28112;
XX
DT   22-APR-2004 (first entry)
XX
DE   Human PRL3 cDNA #2 5' extension #1.
XX
KW   Human; antisense gene therapy; ss; PRL3;
KW   protein tyrosine phosphatase type IVA member 3; colorectal cancer;
KW   diabetes; glucose tolerance; insulin resistance; obesity;
KW   hyperproliferative disorder; cytostatic.
XX
OS   Homo sapiens.
XX
PN   US2003235911-A1.
XX
PD   25-DEC-2003.
XX
PF   20-JUN-2002; 2002US-00177554.
XX
PR   20-JUN-2002; 2002US-00177554.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Dobie KW, Zhang H;
XX
DR   WPI; 2004-070585/07.
XX
PT   New antisense oligonucleotide, comprising a sequence targeted to a
PT   nucleic acid encoding protein tyrosine phosphatase type IVA member 3 (PRL
PT   -3), useful for preparing a composition for treating hyperproliferative
PT   disorders, e.g., cancer.

```
Db    345 CTGGAGTTGGTTCAGTTCAAGTTCATTCTCCTGCCCTTGGGGGCTTGGGCCCACC 404
Qy     96 TCTGAGTGAAGGGGGCTGTGTCTGCC...TTGAGTTTTCTTTGC 155
Db    405 TCTGAGTGAAGGGGGCTGTGTCTGCC...TTGAGTTTTCTTTGC 464
Qy    156 GTCCAGCTCTGGACACTGCT... 215
Db    465 GTCCAGCTCTGGACACTGCT... 524
Qy    216 TGAGCTTTTTTGGTGTGTTCTTTTTATTTTTATTTTTTATGACTATCCAGCTCTGAGAG 275
Db    525 TGAGCTTTTTTGGTGTGTTCTTTTTATTTTTATTTTTTATGACTATCCAGCTCTGAGAG 584
Qy    276 ACGGGAGTTTGGAGTTGGAGTTGCCCGCTTTACTTTGGGGGGGTATGGGGGTGGGTGTTT 335
Db    585 ACGGGAGTTTGGAGTTGGAGTTGCCCGCTTTACTTTGGGGGGGTATGGGGGTGGGTGTTT 644
Qy    336 TGTTCCTTTTCTTTTTTTAAGAGTTGGGTTTTCTTTTTTTAATTATCCAAACAGTGGGCAGC 395
Db    645 TGTTCCTTTTCTTTTTTTAAGAGTTGGGTTTTCTTTTTTTAATTATCCAAACAGTGGGCAGC 704
Qy    396 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGCGGGGTATGGGGGTGGGTTTTT 455
Db    705 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGCGGGGTATGGGGGTGGGTTTTT 764
Qy    456 AAATCTCGTTTCTTCTTGGACAAGCACAGGGATCTCGTTCGTTCTCCTCATTTTTGGGGGTG 515
Db    765 AAATCTCGTTTCTTCTTGGACAAGCACAGGGATCTCGTTCGTTCTCCTCATTTTTGGGGGTG 824
Qy    516 TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCCCTTCCAGTCCCTTCGCCTGCCGGGCC 575
Db    825 TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCCCTTCCAGTCCCTTCGCCTGCCGGGCC 884
Qy    576 CGTCGGGAGGCGCCATG 592
Db    885 CGTCGGGAGGCGCCATG 901
```

Db   736 TGTTCCTTTTCTTTTTAAGAGTTGGGGTTTCTTTTTTAATTATCCAAACAGTGGGCAGC 795
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   396 TTCCCCCCACCCACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGGTGGGGTTTT 455
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   796 TTCCTCCCCACCCACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGGTGGGGTTTT 855

Qy   456 AAATCTCGTTCTTCTTGGACAAGCACAGGGATCTCGTTCTTCCTCATTTTTTGGGGTGTG 515
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   856 AAATCTCGTTCTTCTTGGACAAGCACAGGGATCTCGTTCTTCCTCATTTTTTGGGGTGTG 915

Qy   516 TGGGGACTTCTCAGGTGCGTGTCCCCAGCCTTCTCTGCAGTCCCTTCCGCCTGCCCGGCC 575
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   916 TGGGGACTTCTCAGGTGCGTGTCCCCAGCCTTCTCTGCAGTCCCTTCCGCCTGCCCGGCC 975

Qy   576 CGTCGGGAGGC 586
                |||||||||||
Db   976 CGTCGGGAGGC 986

RESULT 8
ADC99125
ID   ADC99125 standard; cDNA; 1859 BP.
XX
AC   ADC99125;
XX
DT   01-JAN-2004 (first entry)
XX
DE   Human KPP cDNA - SEQ ID 78.
XX
KW   anti-HIV; antiallergic; antiinflammatory; antianaemic; antiparkinsonian;
KW   nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;
KW   immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;
KW   antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective;
KW   osteopathic; antiarthritic; antiparasitic; antihelminthic; antipsoriatic;
KW   uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;
KW   virucide; protozoacide; fungicide; fungistatic; kinase; phosphatase; KPP;
KW   cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;
KW   cancer; developmental; mental retardation; neurological;
KW   Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;
KW   diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;
KW   helminthic infection; transgenic; gene therapy; human; ss; gene.
XX
OS   Homo sapiens.
XX
PN   WO200303680-A2.
XX
PD   24-APR-2003.
XX
PF   17-OCT-2002; 2002WO-US033723.
XX
PR   19-OCT-2001; 2001US-0345474P.
PR   02-NOV-2001; 2001US-0343910P.
PR   13-NOV-2001; 2001US-0333098P.
PR   16-NOV-2001; 2001US-0332424P.
PR   30-NOV-2001; 2001US-0334288P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;
PI   Emerling BM, Forsythe IJ, Gandhi AR, Gorvad AE, Griffin JA;
PI   Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lee SY;
PI   Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;
PI   Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;
PI   Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;
PI   Zebarjadian Y;
XX
DR   WPI; 2003-403214/38.
DR   P-PSDB; ADC99073.
XX
PT   New human kinases and phosphatases and polynucleotides, useful for
PT   diagnosing, treating or preventing autoimmune or inflammatory disorders
PT   (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
PT   cancer or hepatitis.

DE   Metastatic colon cancer-specific transcriptional regulatory element.
XX
KW   Human; PRL-3; promoter; transcriptional regulatory element; gene therapy;
KW   colon cancer; metastasis; cytostatic; gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004009790-A2.
XX
PD   29-JAN-2004.
XX
PF   22-JUL-2003; 2003WO-US023032.
PR   22-JUL-2002; 2002US-0397859P.
XX
PA   (CBLL-) CELL GENESYS INC.
XX
PI   Li Y, Yu DC;
XX
DR   WPI; 2004-123388/12.
XX
PT   New colon cancer transcriptional regulatory element (TRE) sequence that
PT   is specific for metastatic colon cancer cells, useful as a promoter for
PT   specific virus replication.
XX
PS   Claim 5; SEQ ID NO 2; 39pp; English.
XX
CC   The present sequence is that of a colon cancer transcriptional regulatory
CC   element (TRE) derived from the human PRL-3 gene in the region upstream of
CC   the translational start codon. The PRL-3 protein tyrosine phosphatase
CC   gene is specifically expressed at a high level in metastatic colon
CC   cancers. The invention provides replication-competent adenoviral vectors
CC   comprising the present sequence operably linked to a gene required for
CC   virus replication. Methods are provided for introducing into a cell an
CC   adenoviral vector comprising a metastatic colon cancer-specific TRE
CC   operably linked to a gene required for virus replication, and host cells
CC   comprising the adenovirus vector. Methods are also provided for
CC   conferring selective cytotoxicity in target colon cancer cells,
CC   particularly metastatic colon cancer cells, by contacting the cells with
CC   an adenovirus vector of the invention, where the vector enters the cell
CC   and propagates virus. By providing for transcriptional initiating
CC   regulation dependent upon transcription factors that are only active in
CC   specific, limited cell types, virus replication is restricted to target
CC   cells.
XX
SQ   Sequence 986 BP; 131 A; 289 C; 289 G; 277 T; 0 U; 0 Other;

Query Match   93.1%; Score 551; DB 12; Length 986;
Best Local Similarity   100.0%; Pred. No. 7.6e-132;
Matches 551; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   36 CTGGAGTTGGTTCAGTTCAGTTCATTCTTCCTCTCGGCCCTTGGGGCCTTGGGGCCCACC   95
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   436 CTGGAGTTGGTTCAGTTCAGTTCATTCTTCCTCTCGGCCCTTGGGGCCTTGGGGCCCACC 495

Qy   96 TCTGAGTGAAGGGGGCTGTCTGCCCATCCACCAAATGTGAGAGAGGGCGCCCCCGGTGTGGG 155
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   496 TCTGAGTGAAGGGGGCTGTCTGCCCATCCACCAAATGTGAGAGAGGGCGCCCCCGGTGTGGG 555

Qy   156 GTCCAGCTCTGGACACTGCTTGGCGGGCCGGGTTCACTTGAGTTTTAAGTTTCTTTGC 215
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   556 GTCCAGCTCTGGACACTGCTTGGCGGGCCGGGTTCACTTGAGTTTTAAGTTTCTTTGC 615

Qy   216 TGAGCTTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG 275
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   616 TGAGCTTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG 675

Qy   276 ACGGGAGTTTGGAGTTGCCCGGCTTTACCTTTGGTTTGGTTGGGTTGGGGGGGCGGCGGGGCTGTTT 335
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   676 ACGGGAGTTTGGAGTTGCCCGGCTTTACCTTTGGTTTGGTTGGGTTGGGGGGGCGGCGGGGCTGTTT 735

Qy   336 TGTTCCTTTTCTTTTTAAGAGTTGGGGTTTCTTTTTTAATTATCCAAACAGTGGGCAGC 395
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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XX
PS   Claim 5; SEQ ID NO 78; 424pp; English.
XX
CC   The invention relates to a novel isolated polypeptide which is a human
CC   kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,
CC   agonists and antagonists are useful for diagnosing, treating or
CC   preventing cell proliferative disorders such as atherosclerosis,
CC   cirrhosis, hepatitis and cancer, developmental disorders e.g. mental
CC   retardation, neurological disorders including Alzheimer's disease and
CC   Parkinson's disease, autoimmune and inflammatory disorders such as
CC   Crohn's disease and diabetes mellitus and finally, viral, bacterial,
CC   fungal, parasitic, protozoan or helminthic infections. Furthermore, the
CC   polynucleotides encoding KPP may be useful for creating transgenic
CC   animals to model human disease, as well as during gene therapy
CC   procedures. The current sequence is that of the human KPP cDNA of the
CC   invention.
XX
SQ   Sequence 1859 BP; 431 A; 488 C; 544 G; 396 T; 0 U; 0 Other;

Query Match             69.4%;  Score 410.6;  DB 10;  Length 1859;
Best Local Similarity   99.0%;  Pred. No. 1.4e-95;
Matches  413;  Conservative   0;  Mismatches   4;  Indels   0;  Gaps   0;

Qy       176 TGGCGGCCGGGTCACTTGAGTTTTAAGTTTCTTTGCTGAGCTTTTTTGTTGTTCT 235
             ||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db         1 TGGCGGCCGGGTCACTTGAGTTTGGAGTCGTCTTTGCTGAGCTTTTTTGTTGTTCT 60

Qy       236 TTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGCCC 295
             |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db        61 TTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGCCC 120

Qy       296 GCTTTACTTTGGTTGGGTTGGGGGTTGGGGGTTGGGGGCTCGTTTTTGTTCCTTTTTTAAG 355
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GCTTTACTTTGGTTGGGTTGGGGGTTGGGGGTTGGGGGCTCGTTTTTGTTCCTTTTTTAAG 180

Qy       356 AGTTGGGTTTCTTTTTTAATTATCCAAACAGTGGCAGCAGCTTCCTCCCCCACACCCAAGT 415
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 AGTTGGGTTTCTTTTTTAATTATCCAAACAGTGGCAGCAGCTTCCTCCCCCACACCCAAGT 240

Qy       416 ATTTGCACAATATTTGTGCGGGGATGGGGGGTGGGTTTTAAATCTCGTTTCTTCTTGGAC 475
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 ATTTGCACAATATTTGTGCGGGGATGGGGGGTGGGTTTTAAATCTCGTTTCTTCTTGGAC 300

Qy       476 AAGCACAGGGATCTCGTTCTCCTCATTTTTGGGGGTGTGTGGGGGACTTCTCCAGGTCGTG 535
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 AAGCACAGGGATCTCGTTCTCCTCATTTTTGGGGGTGTGTGGGGGACTTCTCCAGGTCGTG 360

Qy       536 TCCCCAGCCTTCTCCTGCGAGTCCCTGCCCCTGCCCGCGGGAGGGGCCATG 592
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 TCCCCAGCCTTCTCCTGCGAGTCCCTGCCCCTGCCCGCGGGAGGGGCCATG 417


RESULT 9
ADN95384
ID   ADN95384 standard; DNA; 1320 BP.
XX
AC   ADN95384;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human BEC/LEC-related gene sequence SeqID307.
XX
KW   growth; differentiation; blood endothelial cell; BEC;
KW   lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
KW   lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;
KW   vasotropic; antiinflammatory; gene therapy; endothelial cell disorder;
KW   inflammatory disease; cancer metastasis; lymphatic system; gene; ds;
KW   human.
XX
OS   Homo sapiens.
XX
PN   WO2003080640-A1.
XX
```

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PD   02-OCT-2003.
XX
PF   07-MAR-2003; 2003WO-US006900.
XX
PR   07-MAR-2002; 2002US-0363019P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (LICN ) LICENTIA LTD.
XX
PI   Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;
XX
DR   WPI; 2003-876899/81.
DR   P-PSDB; ADN95383.
XX
PS   Example 1; SEQ ID NO 307; 176pp; English.
XX
CC   This invention relates to a method of differentially modulating the
CC   growth or differentiation of blood endothelial cells (BEC) or lymphatic
CC   endothelial cells (LEC) comprises contacting endothelial cells with a
CC   composition comprising an agent that differentially modulates blood or
CC   lymphatic endothelial cells. Treating hereditary lymphoedema comprises
CC   identifying a human subject with lymphoedema and with a mutation in at
CC   least one allele of a gene encoding a LEC protein, where the mutation
CC   correlates with lymphoedema in human subjects, and with the proviso that
CC   the LEC protein is not VEGF-3; and administering to the subject a
CC   composition comprising a lymphatic growth agent selected from VEGF-C or
CC   VEGF-D polypeptides and polynucleotides. The invention may be useful for
CC   the development of compounds with an antiangiogenic, cytostatic,
CC   vasotropic or antiinflammatory activity or for gene therapy. The method
CC   is useful in modulating the growth or differentiation of blood
CC   endothelial cells or lymphatic endothelial cells, in treating hereditary
CC   lymphoedema, in screening for an endothelial cell disorder or
CC   predisposition to the disorder or in monitoring the efficacy or toxicity
CC   of a drug on endothelial cells. The agent is useful in manufacturing a
CC   medicament for the differential modulation of blood vessel endothelial
CC   cell or lymphatic vessel endothelial cell growth or differentiation. The
CC   lymphatic growth agent may also be used in manufacturing a medicament for
CC   the treatment of hereditary lymphoedema resulting from a mutation in a
CC   LEC gene or of other diseases involving the lymphatic vessels, such as
CC   various inflammatory diseases and cancer metastasis via the lymphatic
CC   system. The present sequence is that of a human LEC/BEC differentially
CC   expressed gene which is related to the method of the invention.Note: This
CC   sequence does not appear in the specification but was obtained by the
CC   indexer using the source data given in table 14 of the specification.
XX
SQ   Sequence 1320 BP; 266 A; 388 C; 376 G; 290 T; 0 U; 0 Other;

Query Match             56.9%;  Score 337;  DB 11;  Length 1320;
Best Local Similarity  100.0%;  Pred. No. 1.2e-76;
Matches  337;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       256 TGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGCCCGCTTACTTTGGTTGGGTTG 315
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 TGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGCCCGCTTACTTTGGTTGGGTTG 60

Qy       316 GGGGGGCGGGGGCGGGGCGTGTTTGTTCCTTTTTTCTTTTTTAAGAGTTGGGTTTCTTTTTTAA 375
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 GGGGGGCGGGGGCGGGGCGTGTTTGTTCCTTTTTTCTTTTTTAAGAGTTGGGTTTCTTTTTTAA 120

Qy       376 TTATCCAAACAGTGGCAGCTTCCTCCCCCAAGTAGTAGTTGCACAATATTTGTGCG 435
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 TTATCCAAACAGTGGCAGCTTCCTCCCCCAAGTAGTAGTTGCACAATATTTGTGCG 180

Qy       436 GGGTATGGGGGGTGGGTTTTAAATCTCGTTTCTTCTTGGACACACAGGGATCGTTCT 495
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GGGTATGGGGGGTGGGTTTTAAATCTCGTTTCTTCTTGGACACACAGGGATCGTTCT 240

Qy       496 CCTCATTTTTGGGGGTGTGGGGGACTTCCCAGGTCGTGTCCCCAGCCTTCTCCTGCGAGT 555
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CCTCATTTTTGGGGGTGTGGGGGACTTCCCAGGTCGTGTCCCCAGCCTTCTCCTGCGAGT 300

Qy       556 CCCTTCTGCCCCTGCCCGGCCCCGTCGGGAGGCGCCATG 592
             |||||||||||||||||||||||||||||||||||||||
Db            CCCTTCTGCCCCTGCCCGGCCCCGTCGGGAGGCGCCATG 592
```

Db 301 CCCTTCTGCCCTGCCGGCCCGTCGGGAGGCGCCATG 337

Qy 436 GGGTATGGGGTGGGTTTTTAAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCT 495
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 GGGTATGGGGTGGGTTTTTAAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCT 240

Qy 496 CCTCATTTTTGGGGGTGTGGGGACTTCTCAGTTCGTGTCCCCAGCCTTCTCTGCAGT 555
||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 CCTCATTTTTGGGGGTGTGGGGACTTCTCAGTTCGTGTCCCCAGCCTTCTCTGCAGT 300

Qy 556 CCCTTCTGCCCTGCCGGCCCGTCGGGAGGCGCCATG 592
||||||||||||||||||||||||||||||||||
Db 301 CCCTTCTGCCCTGCCGGCCCGTCGGGAGGCGCCATG 337

RESULT 10
ADI28097
ID ADI28097 standard; cDNA; 1321 BP.
XX
AC ADI28097;
XX
DT 22-APR-2004 (first entry)
XX
DE Human protein tyrosine phosphatase, PRL3, variant 1 cDNA.
XX
KW Human; antisense gene therapy; ss; PRL3;
KW protein tyrosine phosphatase type IVA member 3; colorectal cancer;
KW diabetes; glucose tolerance; insulin resistance; obesity;
KW hyperproliferative disorder; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003235911-A1.
XX
PD 25-DEC-2003.
XX
PF 20-JUN-2002; 2002US-00177554.
XX
PR 20-JUN-2002; 2002US-00177554.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dobie KW, Zhang H;
XX
DR WPI; 2004-070585/07.
DR P-PSDB; ADI28833.
XX
PT New antisense oligonucleotide, comprising a sequence targeted to a
PT nucleic acid encoding protein tyrosine phosphatase type IVA member 3 (PRL
PT -3), useful for preparing a composition for treating hyperproliferative
PT disorders, e.g., cancer.
XX
PS Example 13; SEQ ID NO 4; 77pp; English.
XX
CC The invention relates to a compound comprising a sequence comprising 8-80
CC base pairs (bp) targeted to a nucleic acid encoding protein tyrosine
CC phosphatase type IVA member 3 (PRL-3), that specifically hybridises with
CC the nucleic acid encoding PRL-3 and inhibits expression of PRL-3, i.e. is
CC an antisense oligonucleotide (AO). Also included are a composition
CC comprising the compound and a carrier or diluent, inhibiting the
CC expression of PRL-3 in cells or tissues, treating an animal having or
CC suspected of having a disease or condition associated with PRL-3 and
CC screening for an antisense compound. The antisense oligonucleotide is
CC useful for preparing a composition for treating hyperproliferative
CC disorder, particularly cancer ((e.g. colorectal cancer), diabetes,
CC reduced glucose tolerance, insulin resistance and obesity. The present
CC sequence is a Human PRL3 target cDNA sequence.
XX
SQ Sequence 1321 BP; 267 A; 388 C; 376 G; 290 T; 0 U; 0 Other;

Query Match 56.9%; Score 337; DB 12; Length 1321;
Best Local Similarity 100.0%; Pred. No. 1.2e-76;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 256 TGACTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTGCCCGCTTTACTTTGGTTGGGTTG 315
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 TGACTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTGCCCGCTTTACTTTGGTTGGGTTG 60

Qy 316 GGGGGGCGCGGGGGCTGTTTGTTGTTCCTTTTCTTTTTAAGAGTTGGGTTTTCTTTTTAA 375
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 GGGGGGCGCGGGGGCTGTTTGTTGTTCCTTTTCTTTTTAAGAGTTGGGTTTTCTTTTTAA 120

Qy 376 TTATCCAAACAGTGGGCAGCTTCCTCCCCCACACCCAAGTATTTGCACAATATTTGTGCG 435
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 TTATCCAAACAGTGGGCAGCTTCCTCCCCCACACCCAAGTATTTGCACAATATTTGTGCG 180

RESULT 11
ADI57209
ID ADI57209 standard; cDNA; 1321 BP.
XX
AC ADI57209;
XX
DT 22-APR-2004 (first entry)
XX
DE Human PRL-3 encoding cDNA SEQ ID NO:29.
XX
KW cell cycle arrest; CK2-specific siRNA molecule; short interfering RNA;
KW CK2 inhibition; PIM1-specific siRNA molecule; PIM1 inhibition;
KW Hbo1-specific siRNA molecule; Hbo1 inhibition; cytostatic; gene therapy;
KW cancer; proliferative disorder; human; PRL-3; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 335..781
FT /tag= a
FT /product= "PRL-3".
XX
PN WO2004007754-A2.
XX
PD 22-JAN-2004.
XX
PF 14-JUL-2003; 2003WO-US022164.
XX
PR 12-JUL-2002; 2002US-0395443P.
XX
PA (RIGE-) RIGEL PHARM INC.
XX
PI Hitoshi Y, Jenkins Y, Markovtsov V;
XX
DR WPI; 2004-122975/12.
DR P-PSDB; ADI57210.
XX
PT Identifying a compound that modulates cell cycle arrest, useful for
PT developing therapeutic reagents for treating cancer comprising contacting
PT a cell comprising a target polypeptide with the compound.
XX
PS Claim 16; SEQ ID NO 29; 180pp; English.
XX
CC The present invention describes a method for identifying a compound (C)
CC that modulates cell cycle arrest. The method comprises contacting a cell
CC comprising a target polypeptide with the compound (C), where the target
CC polypeptide encoded by the complement of a nucleic acid that hybridises
CC under stringent conditions to a nucleic acid encoding a polypeptide
CC having an amino acid sequence selected from 18 148-1408 amino acid
CC sequences (SEQ ID NO: 2-36, even numbers only). Also described: (1)
CC modulating cell cycle arrest in a subject; (2) a CK2-specific short
CC interfering RNA (siRNA) molecule comprising the sequence: (I)
CC AACATTGAATTAGATCCACGT, where the siRNA molecule is from 21-30 nucleotide
CC base pairs in length; (3) inhibiting expression of a CK2 gene in a cell;
CC (4) a PIM1-specific siRNA molecule comprising the sequence: (II)
CC AAAACTCCGAGTGAACTGGTC, where the siRNA molecule is from 21-30 nucleotide
CC base pairs in length; (5) inhibiting expression of a PIM1 gene in a cell;
CC (6) an Hbo1-specific siRNA molecule comprising the sequence: (III)
CC AACTGAGCAAGTGGTTGATTT, where the siRNA molecule is from 21-30 nucleotide

CC base pairs in length; and (7) inhibiting expression of an Hbo1 gene in a
CC cell. (C) has cytostatic activity, and can be used in gene therapy. The
CC method is useful for identifying a compound (c) that modulates cell cycle
CC arrest. Compounds that modulate cell cycle arrest are useful for
CC developing therapeutic reagents for treating cancer and other
CC proliferative disorders. The present sequence encodes human PRL-3, which
CC is used in the exemplification of the present invention.
XX
SQ Sequence 1321 BP; 267 A; 388 C; 376 G; 290 T; 0 U; 0 Other;

Query Match   56.9%; Score 337; DB 12; Length 1321;
Best Local Similarity 100.0%; Pred. No. 1.2e-76;
Matches 337; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db    1 TGACTATCCAGCTCTGAGAGACGGAGTTGGAGTTGCCCGCTTACTTTGGTTGGGTTG 60

Qy  316 GGGGGGGCGGCGGCGGCTGTTTGTTCCTTTCTTTTTAAGAGTTGGGTTTCTTTTTTAA 375
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GGGGGGGCGGCGGCGGCTGTTTGTTCCTTTCTTTTTAAGAGTTGGGTTTCTTTTTTAA 120

Qy  376 TTATCCAAACAGTGGGCAGCTTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCG 435
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 TTATCCAAACAGTGGGCAGCTTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCG 180

Qy  436 GGGTATGGGGGGTGGGTTTTTAAATCTCGTTCTCTTGGACAAGCACAGGGATCTCGTTCT 495
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 GGGTATGGGGGGTGGGTTTTTAAATCTCGTTCTCTTGGACAAGCACAGGGATCTCGTTCT 240

Qy  496 CCTCATTTTTGGGGGTGTGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTCTGCAGT 555
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Db  241 CCTCATTTTTGGGGGTGTGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTCTGCAGT 300

Qy  556 CCCTTCTGCCCTGCCCGGGGCCCGTCGGGAGGCGCCATG 592
        |||||||||||||||||||||||||||||||||||||||
Db  301 CCCTTCTGCCCTGCCCGGGGCCCGTCGGGAGGCGCCATG 337
```

RESULT 12
ADP21390
ID ADP21390 standard; DNA; 1321 BP.
XX
AC ADP21390;
XX
DT 09-SEP-2004 (first entry)
XX
DE Gene PTP4A3 for screening for cardiac therapeutic preparation.
XX
KW ds; cardiant; gene therapy; cardiac therapeutic preparation;
KW beta-adrenergic receptor antagonist; endothelial receptor antagonist;
KW calcium channel antagonist; phosphodiesterase inhibitor;
KW angiotensin converting enzyme inhibitor; heart failure.
XX
OS Homo sapiens.
XX
PN WO200405894-A2.
XX
PD 17-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US037927.
XX
PR 27-NOV-2002; 2002US-0429379P.
PR 31-DEC-2002; 2002US-0437051P.
PR 31-DEC-2002; 2002US-0437102P.
XX
PA (ARTE-) ARTESIAN THERAPEUTICS INC.
XX
PI Bednarik DP;
XX
DR WPI; 2004-450738/42.
XX
PT Screening potential therapeutic compounds for cardiac therapeutic

PT preparations, useful for treating heart failure in a subject, comprises
PT contacting a sample of cell or tissue with a compound and detecting gene
PT expression level.
XX
PS Claim 10; SEQ ID NO 64; 152pp; English.
XX
CC The invention relates to a method of screening potential therapeutic
CC compounds for cardiac therapeutic preparations by contacting a sample
CC comprising a cell or tissue with a potential therapeutic compound and
CC detecting a level of expression of a gene that codes for a product
CC encoded by a nucleic acid selected from 98 sequences given in the
CC specification and its conservative variants, comparing the level of the
CC expression of the gene to the level of expression of the gene in the
CC absence of the compound, and identifying a potential therapeutic compound
CC for use as a cardiac therapeutic preparation if the potential therapeutic
CC compound affects the level of expression of the gene. The pharmaceutical
CC composition or active agents (i.e., beta-adrenergic receptor antagonist,
CC endothelial receptor antagonist, calcium channel antagonist,
CC phosphodiesterase inhibitor, or angiotensin converting enzyme inhibitor)
CC is useful for treating heart failure in a subject. This sequence
CC represents one of the genes whose expression may be altered by the
CC compounds detected by the screen of the invention.
XX
SQ Sequence 1321 BP; 267 A; 388 C; 376 G; 290 T; 0 U; 0 Other;

Query Match   56.9%; Score 337; DB 12; Length 1321;
Best Local Similarity 100.0%; Pred. No. 1.2e-76;
Matches 337; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy  256 TGACTATCCAGCTCTGAGAGACGGAGTTGGAGTTGCCCGCTTACTTTGGTTGGGTTG 315
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 TGACTATCCAGCTCTGAGAGACGGAGTTGGAGTTGCCCGCTTACTTTGGTTGGGTTG 60

Qy  316 GGGGGGGCGGCGGCGGCTGTTTGTTCCTTTCTTTTTAAGAGTTGGGTTTCTTTTTTAA 375
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GGGGGGGCGGCGGCGGCTGTTTGTTCCTTTCTTTTTAAGAGTTGGGTTTCTTTTTTAA 120

Qy  376 TTATCCAAACAGTGGGCAGCTTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCG 435
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Qy  436 GGGTATGGGGGGTGGGTTTTTAAATCTCGTTCTCTTGGACAAGCACAGGGATCTCGTTCT 495
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Db  181 GGGTATGGGGGGTGGGTTTTTAAATCTCGTTCTCTTGGACAAGCACAGGGATCTCGTTCT 240

Qy  496 CCTCATTTTTGGGGGTGTGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTCTGCAGT 555
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 CCTCATTTTTGGGGGTGTGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTCTGCAGT 300

Qy  556 CCCTTCTGCCCTGCCCGGGGCCCGTCGGGAGGCGCCATG 592
        |||||||||||||||||||||||||||||||||||||||
Db  301 CCCTTCTGCCCTGCCCGGGGCCCGTCGGGAGGCGCCATG 337
```

RESULT 13
ADI28111
ID ADI28111 standard; cDNA; 1396 BP.
XX
AC ADI28111;
XX
DT 22-APR-2004 (first entry)
XX
DE Human protein tyrosine phosphatase, PRL3, variant 2 cDNA.
XX
KW Human; antisense gene therapy; ss; PRL3;
KW protein tyrosine phosphatase type IVA member 3; colorectal cancer;
KW diabetes; glucose tolerance; insulin resistance; obesity;
KW hyperproliferative disorder; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003235911-A1.
XX

PD 25-DEC-2003.
XX
PF 20-JUN-2002; 2002US-00177554.
XX
PR 20-JUN-2002; 2002US-00177554.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dobie KW, Zhang H;
XX
DR WPI; 2004-070585/07.
DR P-PSDB; ADI28335.
XX
PT New antisense oligonucleotide, comprising a sequence targeted to a
PT nucleic acid encoding protein tyrosine phosphatase type IVA member 3 (PRL
PT -3), useful for preparing a composition for treating hyperproliferative
PT disorders, e.g., cancer.
XX
PS Example 15; SEQ ID NO 18; 77pp; English.
XX
CC The invention relates to a compound comprising a sequence comprising 8-80
CC base pairs (bp) targeted to a nucleic acid encoding protein tyrosine
CC phosphatase type IVA member 3 (PRL-3), that specifically hybridises with
CC the nucleic acid encoding PRL-3 and inhibits expression of PRL-3, i.e. is
CC an antisense oligonucleotide (AO). Also included are a composition
CC comprising the compound and a carrier or diluent, inhibiting the
CC expression of PRL-3 in cells or tissues, treating an animal having or
CC suspected of having a disease or condition associated with PRL-3 and
CC screening for an antisense compound. The antisense oligonucleotide is
CC useful for preparing a composition for treating hyperproliferative
CC disorder, particularly cancer ((e.g. colorectal cancer), diabetes,
CC reduced glucose tolerance, insulin resistance and obesity. The present
CC sequence is a Human PRL3 target cDNA sequence.
XX
SQ Sequence 1396 BP; 281 A; 409 C; 400 G; 306 T; 0 U; 0 Other;

Query Match 56.9%; Score 337; DB 12; Length 1396;
Best Local Similarity 100.0%; Pred. No. 1.2e-76;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  256 TGACTATCCAGCTCTGAGAGACGGGAGTTTGCCCGCTTTACTTTGGTTGGGTTG 315
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 TGACTATCCAGCTCTGAGAGACGGGAGTTTGCCCGCTTTACTTTGGTTGGGTTG 60

Qy  316 GGGGGGCGGCGGCGGGCTGTTTTGTTCCTTTTCTTTTTAAGAGTTGGGTTTCTTTTTTAA 375
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GGGGGGCGGCGGCGGGCTGTTTTGTTCCTTTTCTTTTTAAGAGTTGGGTTTCTTTTTTAA 120

Qy  376 TTATCCAAACAGTGGGCAGCTTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCG 435
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Db  121 TTATCCAAACAGTGGGCAGCTTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCG 180

Qy  436 GGGTATGGGGGTGGGTTTTAAATCTCGTTTCTTGGACAAGCACAGGGATCTCGTTCT 495
            |||||||||||||||||||||||||||||||||||||||||||||||
Db  181 GGGTATGGGGGTGGGTTTTAAATCTCGTTTCTTGGACAAGCACAGGGATCTCGTTCT 240

Qy  496 CCTCATTTTTTGGGGGTGTGTGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTCTGCAGT 555
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Db  241 CCTCATTTTTTGGGGGTGTGTGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTCTGCAGT 300

Qy  556 CCCTTCTGCCCTGCCCGGCCCGTCGGGAGGCGCCATG 592
            |||||||||||||||||||||||||||||||||
Db  301 CCCTTCTGCCCTGCCCGGCCCGTCGGGAGGCGCCATG 337
```

RESULT 14
ADN75973
ID ADN75973 standard; DNA; 1396 BP.
XX
AC ADN75973;
XX
DT 01-JUL-2004 (first entry)
XX

DB Human signal transduction-associated DNA SEQ ID 798.
XX
KW small interfering RNA; siRNA; protein-tyrosine-phosphatase; PTP;
KW cytostatic; immunomodulator; antimicrobial; antiinflammatory;
KW antidiabetic; anorectic; cancer; autoimmune disease; infection;
KW inflammation; diabetes; obesity; RNA interference; gene silencing; ds;
KW gene.
XX
OS Homo sapiens.
XX
PN WO2004016735-A2.
XX
PD 26-FEB-2004.
XX
PF 23-MAY-2003; 2003WO-US016632.
XX
PR 23-MAY-2002; 2002US-0383249P.
PR 14-APR-2003; 2003US-0462942P.
XX
PA (CEPT-) CEPTYR INC.
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PI Klinghoffer R, Lewis SP, Tonks NK, Meng T;
XX
DR WPI; 2004-203773/19.
DR P-PSDB; ADN75974.
XX
PT New isolated small interfering RNA (siRNA) polynucleotide useful for
PT treating diseases with aberrant activity of the protein tyrosine
PT phosphatase, such as cancer, autoimmune disease, infection, inflammation,
PT diabetes and obesity.
XX
PS Disclosure; SEQ ID NO 798; 392pp; English.
XX
CC This invention describes novel small interfering RNA (siRNA)
CC polynucleotides capable of interfering with expression of a polypeptide
CC having protein-tyrosine-phosphatase (PTP) activity. The products of the
CC invention have cytostatic, immunomodulator, antimicrobial,
CC antiinflammatory, antidiabetic and anorectic activity. The methods and
CC compositions of the present invention are useful for treating diseases or
CC conditions associated with aberrant expression or activity of the protein
CC tyrosine phosphatase, such as cancer, autoimmune diseases, infection,
CC inflammation, diabetes and obesity. This sequence represents a siRNA
CC directed against dual specificity phosphatase (DSP) expression.
XX
SQ Sequence 1396 BP; 281 A; 409 C; 409 G; 306 T; 0 U; 0 Other;

Query Match 56.9%; Score 337; DB 12; Length 1396;
Best Local Similarity 100.0%; Pred. No. 1.2e-76;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy  256 TGACTATCCAGCTCTGAGAGACGGGAGTTTGCCCGCTTTACTTTGGTTGGGTTG 315
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Db    1 TGACTATCCAGCTCTGAGAGACGGGAGTTTGCCCGCTTTACTTTGGTTGGGTTG 60

Qy  316 GGGGGGCGGCGGCGGGCTGTTTTGTTCCTTTTCTTTTTAAGAGTTGGGTTTCTTTTTTAA 375
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Qy  376 TTATCCAAACAGTGGGCAGCTTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCG 435
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Db  121 TTATCCAAACAGTGGGCAGCTTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCG 180

Qy  436 GGGTATGGGGGTGGGTTTTAAATCTCGTTTCTTGGACAAGCACAGGGATCTCGTTCT 495
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```

```
Db      301 CCCTTCTGCCTGCCGGCCGCCGTCGGGAGGCGCCATG 337

RESULT 15
ADP20802
ID   ADP20802 standard; DNA; 1396 BP.
XX
AC   ADP20802;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human protein tyrosine phosphatase type IVA (Prl-3) gene.
XX
KW   ds; gene; metabolic; anorectic; antilipemic; cardiant; osteopathic;
KW   antiarthritic; antiinflammatory; cytostatic; gene therapy;
KW   Protein tyrosine phosphatase; metabolic disease; metabolic syndrome;
KW   obesity; diabetes; eating disorder; cachexia; hypertension;
KW   coronary heart disease; hypercholesterolemia; dyslipidemia;
KW   osteoarthritis; gallstones; liver fibrosis; transgenic animal.
XX
OS   Homo sapiens.
XX
PN   WO200405O117-A1.
XX
PD   17-JUN-2004.
XX
PF   03-DEC-2003; 2003WO-EP013655.
XX
PR   03-DEC-2002; 2002EP-00026921.
XX
PA   (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
XX
PI   Meise M, Eulenberg K, Nguyen T, Tsetsenis T;
XX
DR   WPI; 2004-450615/42.
DR   P-PSDB; ADP20803.
XX
PT   New pharmaceutical composition comprising a PRL-1 homologous protein or
PT   nucleic acid, and carriers, diluents or/and additives, useful for
PT   treating obesity, hyperlipidemia, osteoarthritis, cell masses.
XX
PS   Disclosure; SEQ ID NO 9; 89pp; English.
XX
CC   The invention relates to a pharmaceutical composition comprising a PRL-1
CC   homologous protein or/and its functional fragment, a nucleic acid
CC   molecule encoding the protein, and/or a modulator/effector of the nucleic
CC   acid molecule or protein, and carriers, diluents or/and additives. The
CC   composition is useful for the manufacture of an agent for detecting
CC   or/and verifying, for the treatment, alleviation and/or prevention of
CC   metabolic diseases or dysfunctions, including metabolic syndrome, obesity
CC   or/and diabetes, as well as related disorders such as eating disorder,
CC   cachexia, hypertension, coronary heart disease, hypercholesterolemia,
CC   dyslipidemia, osteoarthritis, gallstones, or liver fibrosis, in cells,
CC   cell masses, organs and/or subjects in vivo or in vitro. The nucleic acid
CC   molecule and polypeptide are useful for the manufacture of a medicament
CC   for the treatment of obesity, diabetes, or/and metabolic syndrome for
CC   controlling the function of a gene or/and a gene product, which is
CC   influenced or/and modified by a PRL-1 homologous polypeptide, for
CC   identifying substances capable of interacting with a PRL-1 homologous
CC   polypeptide, and for the production of a non-human transgenic animal
CC   which over- or under-expresses the PRL-1. This sequence corresponds to
CC   the human protein tyrosine phosphatase type IVA member 3 i.e. Prl-3 gene.
XX
SQ   Sequence 1396 BP; 281 A; 409 C; 400 G; 306 T; 0 U; 0 Other;

Query Match            56.9%;  Score 337;  DB 12;  Length 1396;
Best Local Similarity  100.0%;  Pred. No. 1.2e-76;
Matches 337;   Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    256 TGACTATCCAGCTCTGAGAGACCGGGAGTTTGCCGCTTTACTTTGGTTGGGTTG 315
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TGACTATCCAGCTCTGAGAGACCGGGAGTTTGCCGCTTTACTTTGGTTGGGTTG 60
```

```
Qy  316 GGGGGGCGGCGGCGGCGGCGTGTTTGTCCTTTCTTTTTTTTTAAGAGTGGGTTTCTTTTTAA 375
        ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   61 GGGGGGCGGCGGCGGCGGCGTGTTTTGTTGTTCCTTTTCTTTTTTTTTAAGAGTGGGTTTCTTTTTAA 120

Qy  376 TTATCCAAACAGTGGGCAGCTTCCTCCCCCACACCCAAGTATTTGCACAATATTTGTGCG 435
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Db  121 TTATCCAAACAGTGGGCAGCTTCCTCCCCCACACCCAAGTATTTGCACAATATTTGTGCG 180

Qy  436 GGGTATGGGGTGGGTTTTAAATCTCGTTTCTTGGACAAGCACAGGGATCTCGTTCT 495
        ||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db  181 GGGTATGGGGTGGGTTTTTAAATCTCGTTTCTTCTTGGACAAGCACAGGGATCTCGTTCT 240

Qy  496 CCTCATTTTTGGGGTGTGTGGGGACTTCTCAGGTCGTGTCCCAGCCTTCTCTGCAGT 555
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 CCTCATTTTTGGGGTGTGTGGGGACTTCTCAGGTCGTGTCCCAGCCTTCTCTGCAGT 300

Qy  556 CCCTTCTGCCTGCCGGGCCGTCGGGAGGCGCCATG 592
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SUMMARIES

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5	557	94.1	2850	8	US-10-474-794-247	Sequence 247, App
6	557	94.1	2850	9	US-10-979-159-247	Sequence 247, App
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11	337	56.9	1321	7	US-10-620-052A-29	Sequence 29, Appl
12	337	56.9	1396	6	US-10-177-554-18	Sequence 18, Appl
13	337	56.9	1396	7	US-11-060-756-798	Sequence 798, App
14	337	56.9	1396	10	US-11-060-756-2935	Sequence 2935, Ap
15	337	56.9	1396	10	US-11-060-756-7207	Sequence 7207, Ap
16	310	52.4	982	9	US-10-305-720-993	Sequence 993, App
17	274.4	46.4	671	6	US-10-177-554-20	Sequence 20, Appl
18	240	40.5	462	8	US-10-723-860-203	Sequence 203, App
19	240	40.5	1006	6	US-10-177-554-239	Sequence 239, App
20	221	37.3	773	6	US-10-277-161-71	Sequence 71, Appl
21	139	23.5	1678	6	US-10-177-554-99	Sequence 99, Appl
22	131.4	22.2	3222	6	US-10-177-554-11	Sequence 11, Appl
23	58	9.8	396	7	US-10-021-323-17801	Sequence 17801, A
24	57	9.6	521	8	US-10-425-115-28564	Sequence 28564, A
c 25	55.2	9.3	683	8	US-10-425-115-92182	Sequence 92182, A
c 26	52.8	8.9	363	8	US-10-021-323-270	Sequence 270, App
27	52.8	8.9	1260	8	US-10-363-345A-3493	Sequence 3493, Ap
c 28	52.8	8.9	1260	8	US-10-363-483A-3493	Sequence 3493, Ap
29	52.8	8.9	1260	9	US-10-363-483A-3494	Sequence 3494, Ap
30	52.4	8.9	444	7	US-10-424-599-85480	Sequence 85480, A
c 31	52.2	8.8	374	7	US-10-424-599-4878	Sequence 4878, Ap
32	52	8.8	7758	6	US-10-311-455-1076	Sequence 1076, Ap
33	52	8.8	192	7	US-10-021-323-5189	Sequence 5189, Ap
c 34	51.2	8.6	629	6	US-10-125-968-78	Sequence 78, Appl
35	51	8.6	7698	6	US-10-311-455-1673	Sequence 1673, Ap
36	50.8	8.6	369	8	US-10-425-115-162538	Sequence 162538,
37	50.6	8.5	1025	8	US-10-363-345A-12421	Sequence 12421, A
38	50.4	8.5	1025	9	US-10-363-345A-12422	Sequence 12422, A
c 39	50.4	8.5	1025	9	US-10-363-483A-12421	Sequence 12421, A
40	50.4	8.5	1025	9	US-10-363-483A-12422	Sequence 12422, A
c 41	50.4	8.5	509	8	US-10-363-345A-5391	Sequence 5391, Ap
42	49.2	8.3	509	8	US-10-363-345A-5392	Sequence 5392, Ap
43	49.2	8.3	509	9	US-10-363-483A-5391	Sequence 5391, Ap
c 44	49.2	8.3	509	9	US-10-363-483A-5392	Sequence 5392, Ap
c 45	49.2	8.3	509	9	US-10-363-483A-5392	Sequence 5392, Ap

ALIGNMENTS

RESULT 1
US-10-624-670-1
; Sequence 1, Application US/10624670
; Publication No. US20040126785A1
; GENERAL INFORMATION:
; APPLICANT: Yuanho Li
; APPLICANT: De-Chao Yu
; TITLE OF INVENTION: Metastatic Colon Cancer Specific
; TITLE OF INVENTION: Promoter and Uses Thereof
; FILE REFERENCE: CELL-024
; CURRENT APPLICATION NUMBER: US/10/624,670
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 60/397,859
; PRIOR FILING DATE: 2002-07-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-624-670-1

Query Match   100.0%; Score 592; DB 7; Length 592;
Best Local Similarity   100.0%; Pred. No. 2.8e-154;
Matches 592; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CTATAGGGCACGCGTGGTCGCGACGGCCCGGCTCGGAGGTTGGTTCAGTTCAAGTTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CTATAGGGCACGCGTGGTCGCGACGGCCCGGCTCGGAGGTTGGTTCAGTTCAAGTTCA 60

Qy   61 TTCTTCCTCTGGGCCCTTGGGGGCGGCCCACCTCGAGTGAAGGGGCTGTCTCGCCC 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TTCTTCCTCTGGGCCCTTGGGGGCGGCCCACCTCGAGTGAAGGGGCTGTCTCGCCC 120

Qy   121 ATCCACCAATGTGAGAGAGGGGCGCCCCGTGTGGGGTCCAGCTCTGGACACTGCTTGGCCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ATCCACCAATGTGAGAGAGGGGCGCCCCGTGTGGGGTCCAGCTCTGGACACTGCTTGGCCG 180

Qy   181 GCCGGGGTTCACTTTGAGTTTAAGTTTTCTTTGCTGAGCTTTTTGGTTGTTCTTTTTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GCCGGGGTTCACTTTGAGTTTAAGTTTTCTTTGCTGAGCTTTTTGGTTGTTCTTTTTA 240

Qy   241 TTTTTTGCCTCTTTATGACTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTGCCCGCTTT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TTTTTTGCCTCTTTATGACTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTGCCCGCTTT 300

Matches 557; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   36  CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTGCGCCTTGGGGCCTTGGGGGCCCACC   95
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  480  CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTGCGCCTTGGGGCCTTGGGGGCCCACC  539

Qy   96  TCTGAGTGAAGGGGGCTGTCTGCGCCATCCACCAATGTGGAGAGGAGCGCCCCGGTGTGGG  155
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  540  TCTGAGTGAAGGGGGCTGTCTGCGCCATCCACCAATGTGGAGAGGAGCGCCCCGGTGTGGG  599

Qy  156  GTCCAGCTCTGGACACTGCTTGGGCGGCCGGGTTCACTTGAGTTTTTCTTTGC  215
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  600  GTCCAGCTCTGGACACTGCTTGGGCGGCCGGGTTCACTTGAGTTTTTCTTTGC  659

Qy  216  TGAGCTTTTTGGTTGTCTTTTATTTTGCCTCTTATTTTTGCCTCTTATGACTATCCAGCTCTGAGAG  275
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  660  TGAGCTTTTTGGTTGTCTTTTATTTTGCCTCTTATTTTTGCCTCTTATGACTATCCAGCTCTGAGAG  719

Qy  276  ACGGGAGTTGGAGTTGCCCGCTTTACTTGGTTGGTTGGTTGTTTCTTTTTAATTATCCAAACAGTGGGCAGC  335
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  720  ACGGGAGTTGGAGTTGCCCGCTTTACTTGGTTGGTTGGTTGTTTCTTTTTAATTATCCAAACAGTGGGCAGC  779

Qy  336  TGTTCCTTTTCTTTTTTAAGAGTTGGGTTTCTTTTTCTTTTTAATTATCCAAACAGTGGGCAGC  395
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  780  TGTTCCTTTTCTTTTTTAAGAGTTGGGTTTCTTTTTCTTTTTAATTATCCAAACAGTGGGCAGC  839

Qy  396  TTCCTCCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGTGGGGTTTTT  455
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  840  TTCCTCCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGTGGGGTTTTT  899

Qy  456  AAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCCTCCTCATTTTTTGGGGTGTG  515
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  900  AAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCCTCCTCATTTTTTGGGGTGTG  959

Qy  516  TGGGGACTTCTCAGTCGTGTCCCCAGCCTTCTCTGCAGTCCCTTCTGCCCTGCCCGGGCC  575
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  960  TGGGGACTTCTCAGTCGTGTCCCCAGCCTTCTCTGCAGTCCCTTCTGCCCTGCCCGGGCC  1019

Qy  576  CGTCGGGAGGCGCCATG  592
         |||||||||||||||||
Db 1020  CGTCGGGAGGCGCCATG 1036
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RESULT 3

Query Match   94.1%;   Score 557;   DB 8; Length 2181;
Best Local Similarity   100.0%;   Pred. No. 2.5e-144;
Matches 557;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy   36  CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTGCGCCTTGGGGCCTTGGGGGCCCACC   95
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  316  CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTGCGCCCTTGGGGCCTTGGGGGCCCACC  375
```

(Left column — RESULT 2 region)

```
Qy  301  ACTTTGGTTGGGTTGGGGGGGGGGGGGGGGGCGCGGGCTGTGTTTGTTCCTTTTCTTTTTTCTTTTTTAAGAGTTG  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  ACTTTGGTTGGGTTGGGGGGGGGGGGGGGGGCGCGGGCTGTGTTTGTTCCTTTTCTTTTTTCTTTTTTAAGAGTTG  360

Qy  361  GGTTTTCTTTTTTAATTATCCAAACAGTGGCAGCTTCTCCCCCACACCCCAGTATTTG  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  GGTTTTCTTTTTTAATTATCCAAACAGTGGCAGCTTCTCCCCCACACCCCAGTATTTG  420

Qy  421  CACAATATTTGTGCGGGGTATGGGGGTGGGTTTTAAAATCTCGTTTCTCTTGGACAAGCA  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  CACAATATTTGTGCGGGGTATGGGGGTGGGTTTTAAAATCTCGTTTCTCTTGGACAAGCA  480

Qy  481  CAGGGATCCTCGTTCCTCCCATTTTTTGGGGTGTGTGGGGACTTCTCAGTCGTGTCCCC  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481  CAGGGATCCTCGTTCCTCCCATTTTTTGGGGTGTGTGGGGACTTCTCAGTCGTGTCCCC  540

Qy  541  AGCCTTCTCTGCAGTCCCTTCTGCCCTGCCCGGGCCCGTCGGGAGGCGCCATG  592
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541  AGCCTTCTCTGCAGTCCCTTCTGCCCTGCCCGGGCCCGTCGGGAGGCGCCATG  592
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RESULT 2

Query Match   94.1%;   Score 557;   DB 9; Length 1692;
Best Local Similarity   100.0%;   Pred. No. 2.2e-144;

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Qy      96 TCTGAGTGAAGGGGGCTGTCTGCCCATCCACCAATGTGGAGAGAGGGCGCCCCCGGTGTGGG 155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     376 TCTGAGTGAAGGGGGCTGTCTGCCCATCCACCAATGTGGAGAGAGGGCGCCCCCGGTGTGGG 435

Qy     156 GTCCAGCTCTGGACACTGCTTGGGCGGCCGGGTTCACTTGAGTTTTTCTTTGC 215
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     436 GTCCAGCTCTGGACACTGCTTGGGCGGCCGGGTTCACTTGAGTTTTTCTTTGC 495

Qy     216 TGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG 275
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     496 TGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG 555

Qy     276 ACGGGAGTTGGAGTTGCCCGCTTACTTGGTTGGGTTGGGTTGGGTTGGGCGCGGCGGCTGTTT 335
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     556 ACGGGAGTTGGAGTTGCCCGCTTACTTGGTTGGGTTGGGTTGGGTTGGGCGCGGCGGCTGTTT 615

Qy     336 TGTTCCTTTTCTTTTTCTTTTTAAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGC 395
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     616 TGTTCCTTTTCTTTTTCTTTTTAAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGC 675

Qy     396 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGTGGGTTTT 455
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     676 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGTGGGTTTT 735

Qy     456 AAATCTCGTTCTTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTGGGGGTGTG 515
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     736 AAATCTCGTTCTTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTGGGGGTGTG 795

Qy     516 TGGGGACTTCTCAGGTCGTCGTGTCCCCAGCCTTCTTCTGCAGTCCCTTCGCCCGGCC 575
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     796 TGGGGACTTCTCAGGTCGTCGTGTCCCCAGCCTTCTTCTGCAGTCCCTTCGCCCGGCC 855

Qy     576 CGTCGGGAGGCGCCATG 592
           |||||||||||||||||
Db     856 CGTCGGGAGGCGCCATG 872
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RESULT 4
US-09-918-715-247
; Sequence 247, Application US/09918715
; Publication No. US2003001715701
; GENERAL INFORMATION:
;   APPLICANT: Brad St. Croix
;   APPLICANT: Bert Vogelstein
;   APPLICANT: Kenneth Kinzler
;   TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
;   FILE REFERENCE: 1107.00134
;   CURRENT APPLICATION NUMBER: US/09/918,715
;   CURRENT FILING DATE: 2001-08-01
;   PRIOR APPLICATION NUMBER: 60/222,599
;   PRIOR FILING DATE: 2000-08-02
;   PRIOR APPLICATION NUMBER: 60/224,360
;   PRIOR FILING DATE: 2000-08-11
;   PRIOR APPLICATION NUMBER: 60/282,850
;   PRIOR FILING DATE: 2000-04-11
;   NUMBER OF SEQ ID NOS: 358
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 247
;   LENGTH: 2850
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-918-715-247

Query Match   94.1%; Score 557; DB 3; Length 2850;
Best Local Similarity 100.0%; Pred. No. 2.7e-144;
Matches   557; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy      36 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGCCCTTGGGGCTTGGGGCCCACC 95
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     345 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGCCCTTGGGGCTTGGGGCCCACC 404

Qy      96 TCTGAGTGAAGGGGGCTGTCTGCCCATCCACCAATGTGGAGAGAGGGCGCCCCCGGTGTGGG 155
```

```
Db     405 TCTGAGTGAAGGGGGCTGTCTGCCCATCCACCAATGTGGAGAGAGGGCGCCCCCGGTGTGGG 464

Qy     156 GTCCAGCTCTGGACACTGCTTGGGCGGCCGGGTTCACTTGAGTTTTTCTTTGC 215
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     465 GTCCAGCTCTGGACACTGCTTGGGCGGCCGGGTTCACTTGAGTTTTTCTTTGC 524

Qy     216 TGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG 275
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     525 TGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAG 584

Qy     276 ACGGGAGTTGGAGTTGCCCGCTTACTTGGTTGGGTTGGGTTGGGCGCGGCGGCTGTTT 335
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     585 ACGGGAGTTGGAGTTGCCCGCTTACTTGGTTGGGTTGGGTTGGGCGCGGCGGCTGTTT 644

Qy     336 TGTTCCTTTTCTTTTTCTTTTTAAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGC 395
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     645 TGTTCCTTTTCTTTTTCTTTTTAAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGC 704

Qy     396 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGTGGGTTTT 455
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     705 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGTGGGTTTT 764

Qy     456 AAATCTCGTTCTTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTGGGGGTGTG 515
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     765 AAATCTCGTTCTTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTGGGGGTGTG 824

Qy     516 TGGGGACTTCTCAGGTCGTCGTGTCCCCAGCCTTCTTCTGCAGTCCCTTCGCCCGGCC 575
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     825 TGGGGACTTCTCAGGTCGTCGTGTCCCCAGCCTTCTTCTGCAGTCCCTTCGCCCGGCC 884

Qy     576 CGTCGGGAGGCGCCATG 592
           |||||||||||||||||
Db     885 CGTCGGGAGGCGCCATG 901
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RESULT 5
US-10-474-794-247
; Sequence 247, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
;   APPLICANT: Carson-Walter, Eleanor
;   APPLICANT: St. Croix, Brad
;   APPLICANT: Vogelstein, Bert
;   APPLICANT: Kinzler, Kenneth
;   TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
;   FILE REFERENCE: 1107.00179
;   CURRENT APPLICATION NUMBER: US/10/474,794
;   CURRENT FILING DATE: 2003-10-14
;   PRIOR APPLICATION NUMBER: 60/282,850
;   PRIOR FILING DATE: 2001-04-11
;   PRIOR APPLICATION NUMBER: 60/308,829
;   PRIOR FILING DATE: 2001-08-01
;   NUMBER OF SEQ ID NOS: 359
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 247
;   LENGTH: 2850
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-474-794-247

Query Match   94.1%; Score 557; DB 8; Length 2850;
Best Local Similarity 100.0%; Pred. No. 2.7e-144;
Matches   557; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy      36 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGCCCTTGGGGCTTGGGGCCCACC 95
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     345 CTGGAGTTGGTTCAGTTCAAGTTCATTCTTCCTCTGCCCTTGGGGCTTGGGGCCCACC 404

Qy      96 TCTGAGTGAAGGGGGCTGTCTGCCCATCCACCAATGTGGAGAGAGGGCGCCCCCGGTGTGGG 155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     405 TCTGAGTGAAGGGGGCTGTCTGCCCATCCACCAATGTGGAGAGAGGGCGCCCCCGGTGTGGG 464
```

Qy 156 GTCCAGCTCTGGACACTGCTTGGCGGCCGGGTTCACTTTGAGTTTTTAAGTTTTCTTTGC 215
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 465 GTCCAGCTCTGGACACTGCTTGGCGGCCGGGTTCACTTTGAGTTTTTAAGTTTTCTTTGC 524

Qy 216 TGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTATGACTATCCAGCTCTGAGAG 275
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 525 TGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTATGACTATCCAGCTCTGAGAG 584

Qy 276 ACGGGAGTTGGAGTTGCCCGCTTTACTTTGGTTGGGTTGGGTTGGGGCGGGGCGGGGCTGTTT 335
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 585 ACGGGAGTTGGAGTTGCCCGCTTTACTTTGGTTGGGTTGGGTTGGGGCGGGGCGGGGCTGTTT 644

Qy 336 TGTTCCTTTTCTTTTTAAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGC 395
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 645 TGTTCCTTTTCTTTTTAAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGC 704

Qy 396 TTCCTCCCCACACCCAAGTATTTGCACAATATTGTGCGGGGTATGGGGGTGGGTTTTT 455
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 705 TTCCTCCCCACACCCAAGTATTTGCACAATATTGTGCGGGGTATGGGGGTGGGTTTTT 764

Qy 456 AAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTTGGGGGTGTG 515
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 765 AAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTTGGGGGTGTG 824

Qy 516 TGGGGACTTCTCAGTGCGTGTCCCCAGCCTTCCTTCGCCCTGCCCTCTGCGCCGGGCC 575
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 825 TGGGGACTTCTCAGTGCGTGTCCCCAGCCTTCCTTCGCCCTGCCCTCTGCGCCGGGCC 884

Qy 576 CGTCGGGAGGCGCCATG 592
         |||||||||||||||||
Db 885 CGTCGGGAGGCGCCATG 901

RESULT 6
US-10-979-159-247
; Sequence 247, Application US/10979159
; Publication No. US2005142138A1
; GENERAL INFORMATION:
;   APPLICANT: Brad St. Croix
;   APPLICANT: Bert Vogelstein
;   APPLICANT: Kenneth Kinzler
;   TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
;   FILE REFERENCE: 1107.00134
;   CURRENT APPLICATION NUMBER: US/10/979,159
;   CURRENT FILING DATE: 2004-11-03
;   PRIOR APPLICATION NUMBER: US/09/918,715
;   PRIOR FILING DATE: 2001-08-01
;   PRIOR APPLICATION NUMBER: 60/222,599
;   PRIOR FILING DATE: 2000-08-02
;   PRIOR APPLICATION NUMBER: 60/224,360
;   PRIOR FILING DATE: 2000-08-11
;   PRIOR APPLICATION NUMBER: 60/282,850
;   PRIOR FILING DATE: 2000-04-11
;   NUMBER OF SEQ ID NOS: 358
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 247
;   LENGTH: 2850
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-979-159-247

Query Match   94.1%;   Score 557; DB 9; Length 2850;
Best Local Similarity 100.0%;   Pred. No. 2.7e-144;
Matches 557; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   36 CTGGAGTTGGTTCAGTTCAGTTCAAGTTCATTCTTCCTCGGCCCTTGGGGCTTGGGCGCCCACC   95
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 345 CTGGAGTTGGTTCAGTTCAGTTCAAGTTCATTCTTCCTCGGCCCTTGGGGCTTGGGCGCCCACC 404

Qy   96 TCTGAGTGAAGGGGGCGTGTCGCCATCCACCAATGTGAGAGGCGCCCCCGGTGTGGG 155
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 405 TCTGAGTGAAGGGGGCGTGTCGCCATCCACCAATGTGAGAGGCGCCCCCGGTGTGGG 464

Qy 156 GTCCAGCTCTGGACACTGCTTGGCGGCCGGGTTCACTTTGAGTTTTTAAGTTTTCTTTGC 215
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 465 GTCCAGCTCTGGACACTGCTTGGCGGCCGGGTTCACTTTGAGTTTTTAAGTTTTCTTTGC 524

Qy 216 TGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTATGACTATCCAGCTCTGAGAG 275
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 525 TGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTATGACTATCCAGCTCTGAGAG 584

Qy 276 ACGGGAGTTGGAGTTGCCCGCTTTACTTTGGTTGGGTTGGGTTGGGGCGGGGCGGGGCTGTTT 335
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 585 ACGGGAGTTGGAGTTGCCCGCTTTACTTTGGTTGGGTTGGGTTGGGGCGGGGCGGGGCTGTTT 644

Qy 336 TGTTCCTTTTCTTTTTAAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGC 395
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 645 TGTTCCTTTTCTTTTTAAGAGTTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGC 704

Qy 396 TTCCTCCCCACACCCAAGTATTTGCACAATATTGTGCGGGGTATGGGGGTGGGTTTTT 455
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 705 TTCCTCCCCACACCCAAGTATTTGCACAATATTGTGCGGGGTATGGGGGTGGGTTTTT 764

Qy 456 AAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTTGGGGGTGTG 515
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 765 AAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTTGGGGGTGTG 824

Qy 516 TGGGGACTTCTCAGTGCGTGTCCCCAGCCTTCCTTCGCCCTGCCCTCTGCGCCGGGCC 575
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 825 TGGGGACTTCTCAGTGCGTGTCCCCAGCCTTCCTTCGCCCTGCCCTCTGCGCCGGGCC 884

Qy 576 CGTCGGGAGGCGCCATG 592
         |||||||||||||||||
Db 885 CGTCGGGAGGCGCCATG 901

RESULT 7
US-10-177-554-19
; Sequence 19, Application US/10177554
; Publication No. US20030235911A1
; GENERAL INFORMATION:
;   APPLICANT: Kenneth W. Doble
;   APPLICANT: Hong Zhang
;   TITLE OF INVENTION: ANTISENSE MODULATION OF PRL-3 EXPRESSION
;   FILE REFERENCE: RTS-0370
;   CURRENT APPLICATION NUMBER: US/10/177,554
;   CURRENT FILING DATE: 2002-06-20
;   NUMBER OF SEQ ID NOS: 239
; SEQ ID NO 19
;   LENGTH: 909
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-177-554-19

Query Match   93.8%;   Score 555; DB 6; Length 909;
Best Local Similarity   99.6%;   Pred. No. 6.4e-144;
Matches 555; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy   36 CTGGAGTTGGTTCAGTTCAGTTCAAGTTCATTCTTCCTCGGCCCTTGGGGCTTGGGCGCCCACC   95
         |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db 317 CTGGAGTTGGTTCAGTTCAGTTCAAGTTCATTCTTCCTCGGCCCTTGGGGCTTGGGCGCCCACC 376

Qy   96 TCTGAGTGAAGGGGGCGTGTCGCCATCCACCAATGTGAGAGGCGCCCCCGGTGTGGG 155
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 377 TCTGAGTGAAGGGGGCGTGTCGCCATCCACCAATGTGAGAGGCGCCCCCGGTGTGGG 436

Qy 156 GTCCAGCTCTGGACACTGCTTGGCGGCCGGGTTCACTTTGAGTTTTTAAGTTTTCTTTGC 215
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 437 GTCCAGCTCTGGACACTGCTTGGCGGCCGGGTTCACTTTGAGTTTTTAAGTTTTCTTTGC 496

Qy 216 TGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTATGACTATCCAGCTCTGAGAG 275
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 497 TGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTATGACTATCCAGCTCTGAGAG 556

Qy 276 ACGGGAGTTGGAGTTGCCCGCTTTACTTTGGTTGGGTTGGGTTGGGGCGGGGCGGGGCTGTTT 335

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Db  557 ACGGAGTATGGAGTTGCCCGCTTTACTTTGGTTGGTTGGGTGGGGCCGGCGGGCTGTGTT 616
        |||||||||||||||    |||||||||
Qy  336 TGTTCCTTTCTTTTCTTTTTTAAGAGTTGGGTTTCTTTTTTCTTTTTTAATTATTCCAAACAGTGGGCAGC 395
        ||||||||||||||||||||||||||||||||||||||||||
Db  617 TGTTCCTTTCTTTTCTTTTTTAAGAGTTGGGTTTCTTTTTTCTTTTTTAATTATTCCAAACAGTGGGCAGC 676

Qy  396 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGGTGGGTTTT 455
        |||||||||||||||||||||
Db  677 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGGTGGGTTTT 736

Qy  456 AAATCTGTTTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTGGGGGTGTG 515
        ||||||||||||||||||||||
Db  737 AAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTGGGGGTGTG 796

Qy  516 TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCCCTTGCCCTGCCCTGCCGGGCC 575
        ||||||||||||||||||||::||||||
Db  797 TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTCTGCAGTYCCTTCTCGCCGGGCC 856

Qy  576 CGTCGGGAGGCGCCATG 592
        |||||||||||||||
Db  857 CGTCGGGAGGCGCCATG 873
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RESULT 8
US-10-624-670-2
; Sequence 2, Application US/10624670
; Publication No. US2004012678A1
; GENERAL INFORMATION:
; APPLICANT: Yuanho Li
; APPLICANT: De-Chao Yu
; TITLE OF INVENTION: Metastatic Colon Cancer Specific
; TITLE OF INVENTION: Promoter and Uses Thereof
; FILE REFERENCE: CELL-024
; CURRENT APPLICATION NUMBER: US/10/624,670
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 60/397,859
; PRIOR FILING DATE: 2002-07-22
; SOFTWARE: FastSEQ for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 986
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-624-670-2

Query Match   93.1%; Score 551; DB 7; Length 986;
Best Local Similarity   100.0%; Pred. No. 8.6e-143;
Matches 551; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy  396 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGGTGGGTTTT 455
        |||||||||||    |||||||||
Db  796 TTCCTCCCCACACCCAAGTATTTGCACAATATTTGTGCGGGGTATGGGGGTGGGTTTT 855

Qy  456 AAATCTGTTTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTGGGGGTG 515
        ||||||||||||||||||||
Db  856 AAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCTCCTCATTTTTGGGGGTG 915

Qy  516 TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTCTGCAGTCCCTTCTCGCCGGCC 575
        ||||||||||||||||||||
Db  916 TGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCTCTGCAGTCCCTTCTCGCCGGGCC 975

Qy  576 CGTCGGGAGGC 586
        |||||||||||
Db  976 CGTCGGGAGGC 986
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RESULT 9
US-10-491-467-78
; Sequence 78, Application US/10491467
; Publication No. US2005018656A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; BANDMAN, Olga;
; APPLICANT: BAUGHN, Mariah R.; BECHA, Shanya D.;
; APPLICANT: BOROWSKY, Mark L.; DUGGAN, Brendan M.;
; APPLICANT: EMERLING, Brooke M.; FORSYTHE, Ian J.;
; APPLICANT: GANDHI, Ameena R.; GORVAD, Ann E.;
; APPLICANT: GRIFFIN, Jennifer A.; GURURAJAN, Rajagopal;
; APPLICANT: HAFALIA, April J.A.; KHAN, Farrah A.;
; APPLICANT: LAL, Preeti G.; LEE, Ernestine A.;
; APPLICANT: LEE, Soo Yeun; LINDQUIST, Erika A.;
; APPLICANT: LU, Dyung Aina M.; LU, Yan;
; APPLICANT: MARQUIS, Joseph P.; NGUYEN, Danniel B.;
; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi;
; APPLICANT: RECIPON, Shirley A.; RICHARDSON, Thomas W.;
; APPLICANT: SWARNAKAR, Anita; TANG, Y. Tom;
; APPLICANT: THORNTON, Michael B.; TRAN, Uyen K.;
; APPLICANT: CHAWLA, Narinder K.; WARREN, Bridget A.;
; APPLICANT: YANG, Junming; YAO, Monique G.;
; APPLICANT: YUE, Henry; ZEBARJADIAN, Yeganeh
; TITLE OF INVENTION: KINASES AND PHOSPHATASES
; FILE REFERENCE: PF-1244 USN
; CURRENT APPLICATION NUMBER: US/10/491,467
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: PCT/US02/33723
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/345,474
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/343,910
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US 60/333,098
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/332,424
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/334,288
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PERL Program
; SEQ ID NO 78
; LENGTH: 1859
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7504546CB1
US-10-491-467-78

Query Match   69.4%; Score 410.6; DB 9; Length 1859;
Best Local Similarity   99.0%; Pred. No. 1.3e-103;
Matches 413; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

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Qy  176 TGGCGGCCGGGTCACTTGAGTTTTAAGTTTTCTTTGCTGAGCTTTTTTGTTGTTCT 235
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Qy   36 CTGGAGTGGTTGGTTCAAGTTCATTCTTCCTCTGCCCTTGGGGCCCACC 95
        |||||||||||||||||||||||||||||||||||||||||||||
Db  436 CTGGAGTGGTTGGTTCAAGTTCATTCTTCCTCTGCCCTTGGGGCCCACC 495

Qy   96 TCTGAGTGAAGGGGGCTGTCTGCCCATCCACCAATGTGGAGAGAGGCGCCCCCCGGTGTGGG 155
        |||||||||||||||||||||||||||||||||
Db  496 TCTGAGTGAAGGGGGCTGTCTGCCCATCCACCAATGTGGAGAGAGGCGCCCCCCGGTGTGGG 555

Qy  156 GTCCAGCTCTGACACTGCTTGCGCGCCGGGTTCACTTGAGTTTTCTTTGC 215
        |||||||||||||||||||||||
Db  556 GTCCAGCTCTGACACTGCTTGCGCGCCGGGTTCACTTGAGTTTTCTTTGC 615

Qy  216 TGAGCTTTTTGTTTCTTTTGTTGTTCTTTTATTTTTTGCCTCTTCTTATGACTATCCAGCTCTGAGAG 275
        |||||||||||||||||||||||||
Db  616 TGAGCTTTTTGTTTCTTTTATTTTTTGCCTCTTCTTATGACTATCCAGCTCTGAGAG 675

Qy  276 ACGGGAGTTTGGAGTTGCCCGCGTTTGCTTACTTTGGTTGGTTGGGTGGGGCGGCGGGCTGTTT 335
        ||||||||||||||||||||||||
Db  676 ACGGGAGTTGGAGTTGCCCCGTTTACTTTGGTTGGTTGGGTGGGGCGGCGGGCTGTTT 735

Qy  336 TGTTCCTTTCTTTTCTTTTTTAAGAGTTGGGTTTCTTTTTTCTTTTTTAATTATTCCAAACAGTGGGCAGC 395
        ||||||||||||||||||||||||
Db  736 TGTTCCTTTCTTTTCTTTTTTAAGAGTTGGGTTTCTTTTTTCTTTTTTAATTATTCCAAACAGTGGGCAGC 795
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Left column:

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Db            ||||||||||||||  |||||||  |||   ||||||||||||||
          1 TGGGCGCCGGGTCACTTGAGTTTGGAGTCGTCTTGCTGGAGTCGTTTTGGTTGTTTCT    60

Qy      236 TTTTATTTTTTGCCTCTTCTTTATGACTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTGCCC   295
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TTTTATTTTTTGCCTCTTCTTTATGACTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTGCCC   120

Qy      296 GCTTTACTTGGTTGGTTGGGGTTGGGGGGCGGCGGCGGCGGTCTGTTTGTTCCTTTTCTTTTTTTAAG   355
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GCTTTACTTGGTTGGTTGGGGGTTGGGGGGCGGCGGCGGCGGTCTGTTTGTTCCTTTTCTTTTTTTAAG   180

Qy      356 AGTTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCCCCCACACCCCAAGT   415
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 AGTTGGGTTTCTTTTTAATTATCCAAACAGTGGGCAGCTTCCTCCCCCACACCCCAAGT   240

Qy      416 ATTTGCACAATATTTGTGCGGGTATGGGGTGGTTTTTAAATCTCGTTTCTCGTTGGAC   475
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 ATTTGCACAATATTTGTGCGGGTATGGGGTGGTTTTTAAATCTCGTTTCTCGTTGGAC   300

Qy      476 AAGCACAGGGATCTCGTTCTCCTCATTTTTGGGGTGTGTGGGACTTCTCAGGTCGTG   535
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 AAGCACAGGGATCTCGTTCTCCTCATTTTTGGGGTGTGTGGGACTTCTCAGGTCGTG   360

Qy      536 TCCCCCAGCCTTCCTCTGCAGTCCCTTCCCTTGCCCTGCCCGGGCCCGTCGGGAGGGCGGCCATG   592
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 TCCCCAGCCTTCCTCTGCAGTCCCTTCCCTTGCCCTGCCCGGGCCCGTCGGGAGGGCGGCCATG   417
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RESULT 10
US-10-177-554-4
; Sequence 4, Application US/10177554
; Publication No. US20030235911A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Hong Zhang
; TITLE OF INVENTION: ANTISENSE MODULATION OF PRL-3 EXPRESSION
; FILE REFERENCE: RTS-0370
; CURRENT APPLICATION NUMBER: US/10/177,554
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 239
; SEQ ID NO 4
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (335)...(781)
US-10-177-554-4

Query Match   56.9%; Score 337; DB 6; Length 1321;
Best Local Similarity   100.0%; Pred. No. 3.4e-83;
Matches   337; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy      256 TGACTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTGCCCGCTTTACTTGGTTGGGGTTG   315
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 TGACTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTGCCCGCTTTACTTGGTTGGGGTTG    60

Qy      316 GGGGGGCGGCGGCGGCGGTCTGTTTGTTCCTTTTCTTTTTTAAGAGTTGGGTTTCTTTTTAA   375
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 GGGGGGCGGCGGCGGCGGTCTGTTTGTTCCTTTTCTTTTTTAAGAGTTGGGTTTCTTTTTAA   120

Qy      376 TTATCCAAACAGTGGGCAGCTTCCTCCCCCACACCCCAAGTATTTGCACAATATTTGTGCG   435
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TTATCCAAACAGTGGGCAGCTTCCTCCCCCACACCCCAAGTATTTGCACAATATTTGTGCG   180

Qy      436 GGGTATGGGGTGGTTTTTAAATCTCGTTTCTCGTTGGACAAGCAGCACAGGGATCTCGTTCT   495
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GGGTATGGGGTGGTTTTTAAATCTCGTTTCTCGTTGGACAAGCAGCACAGGGATCTCGTTCT   240

Qy      496 CCTCATTTTTTGGGGGTGTGTGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCCTCTGCAGT   555
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CCTCATTTTTTGGGGGTGTGTGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCCTCTGCAGT   300
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Right column:

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Qy      556 CCCTTCTGCCCTGCCCGGGCCCGTCGGGAGGGCGGCCATG   592
            ||||||||||||||||||||||||||||||||
Db      301 CCCTTCTGCCCTGCCCGGGCCCGTCGGGAGGGCGGCCATG   337
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RESULT 11
US-10-620-052A-29
; Sequence 29, Application US/10620052A
; Publication No. US20040126784A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Jenkins, Yonchu
; APPLICANT: Markovtsov, Vadim
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: Modulators of Cellular Proliferation
; FILE REFERENCE: 021044-004010US
; CURRENT APPLICATION NUMBER: US/10/620,052A
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 60/395,443
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 29
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: potentially prenylated protein tyrosine
; OTHER INFORMATION: phosphatase (PRL-3), protein tyrosine phosphatase
; OTHER INFORMATION: type IVA, member 3, isoform 2, transcript variant
; OTHER INFORMATION: 2 (PTP4A3)
US-10-620-052A-29

Query Match   56.9%; Score 337; DB 7; Length 1321;
Best Local Similarity   100.0%; Pred. No. 3.4e-83;
Matches   337; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy      256 TGACTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTGCCCGCTTTACTTGGTTGGGGTTG   315
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 TGACTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTGCCCGCTTTACTTGGTTGGGGTTG    60

Qy      316 GGGGGGCGGCGGCGGCGGCTGTTTGTTCCTTTTCTTTTTTAAGAGTTGGGTTTCTTTTTTAA   375
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 GGGGGGCGGCGGCGGCGGCTGTTTGTTCCTTTTCTTTTTTAAGAGTTGGGTTTCTTTTTTAA   120

Qy      376 TTATCCAAACAGTGGGCAGCTTCCTCCCCCACACCCCAAGTATTTGCACAATATTTGTGCG   435
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TTATCCAAACAGTGGGCAGCTTCCTCCCCCACACCCCAAGTATTTGCACAATATTTGTGCG   180

Qy      436 GGGTATGGGGTGGTTTTTAAATCTCGTTTCTCGTTGGACAAGCAGCACAGGGATCTCGTTCT   495
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GGGTATGGGGTGGTTTTTAAATCTCGTTTCTCGTTGGACAAGCAGCACAGGGATCTCGTTCT   240

Qy      496 CCTCATTTTTTGGGGGTGTGTGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCCTCTGCAGT   555
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CCTCATTTTTTGGGGGTGTGTGGGGACTTCTCAGGTCGTGTCCCCAGCCTTCCTCTGCAGT   300

Qy      556 CCCTTCTGCCCTGCCCGGGCCCGTCGGGAGGGCGGCCATG   592
            ||||||||||||||||||||||||||||||||
Db      301 CCCTTCTGCCCTGCCCGGGCCCGTCGGGAGGGCGGCCATG   337
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RESULT 12
US-10-177-554-18
; Sequence 18, Application US/10177554
; Publication No. US20030235911A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Hong Zhang
; TITLE OF INVENTION: ANTISENSE MODULATION OF PRL-3 EXPRESSION
; FILE REFERENCE: RTS-0370
; CURRENT APPLICATION NUMBER: US/10/177,554

; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 239
; SEQ ID NO 18
; LENGTH: 1396
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (335)...(856)
US-10-177-554-18

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Query Match      56.9%;  Score 337;  DB 6;  Length 1396;
Best Local Similarity  100.0%;  Pred. No. 3.5e-83;
Matches  337;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    256 TGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGCCCGCTTTACTTGGTTGGGTTG 315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGCCCGCTTTACTTGGTTGGGTTG 60

Qy    316 GGGGGGGCGGCGGGCGGGGCTGTTTTGTCCTTTGTCCTTTTCTTTTTCTTTTTTTAA 375
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGGGGGGCGGCGGGCGGGGCTGTTTTGTCCTTTGTCCTTTTCTTTTTCTTTTTTTAA 120

Qy    376 TTATCCAAACAGTGGGCAGCTTCCTCCCCACACCCAAGTATTGCACAATATTTGTGCG 435
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TTATCCAAACAGTGGGCAGCTTCCTCCCCACACCCAAGTATTGCACAATATTTGTGCG 180

Qy    436 GGGTATGGGGGTGGTTTTAAATCTCGTTTCTTGGACAAGCACAGGGATCTCGTTCT 495
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GGGTATGGGGGTGGTTTTAAATCTCGTTTCTTGGACAAGCACAGGGATCTCGTTCT 240

Qy    496 CCTCATTTTTGGGGGTGTGTGGGGACTTCTCAGTGTCGTGTCCCCAGCCTTCTCTCGCAGT 555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CCTCATTTTTGGGGGTGTGTGGGGACTTCTCAGTGTCGTGTCCCCAGCCTTCTCTCGCAGT 300

Qy    556 CCCTTCTGCCCTGCCGGGCCCGTCGGGAGGCGCCATG 592
          |||||||||||||||||||||||||||||||||||||
Db    301 CCCTTCTGCCCTGCCGGGCCCGTCGGGAGGCGCCATG 337
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RESULT 13
US-10-444-795B-798
; Sequence 798, Application US/10444795B
; Publication No. US20040077574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 798
; LENGTH: 1396
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-444-795B-798

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Query Match      56.9%;  Score 337;  DB 7;  Length 1396;
Best Local Similarity  100.0%;  Pred. No. 3.5e-83;
Matches  337;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    256 TGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGCCCGCTTTACTTGGTTGGGTTG 315
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGCCCGCTTTACTTGGTTGGGTTG 60

Qy    316 GGGGGGGCGGCGGGCGGGGCTGTTTTGTCCTTTGTCCTTTTCTTTTTCTTTTTTTAA 375
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGGGGGGCGGCGGGCGGGGCTGTTTTGTCCTTTGTCCTTTTCTTTTTCTTTTTTTAA 120
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```
Qy    376 TTATCCAAACAGTGGGCAGCTTCCTCCCCACACCCAAGTATTGCACAATATTTGTGCG 435
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TTATCCAAACAGTGGGCAGCTTCCTCCCCACACCCAAGTATTGCACAATATTTGTGCG 180

Qy    436 GGGTATGGGGGTGGTTTTAAATCTCGTTTCTTGGACAAGCACAGGGATCTCGTTCT 495
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GGGTATGGGGGTGGTTTTAAATCTCGTTTCTTGGACAAGCACAGGGATCTCGTTCT 240

Qy    496 CCTCATTTTTGGGGGTGTGTGGGGACTTCTCAGTGTCGTGTCCCCAGCCTTCTCTCGCAGT 555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CCTCATTTTTGGGGGTGTGTGGGGACTTCTCAGTGTCGTGTCCCCAGCCTTCTCTCGCAGT 300

Qy    556 CCCTTCTGCCCTGCCGGGCCCGTCGGGAGGCGCCATG 592
          |||||||||||||||||||||||||||||||||||||
Db    301 CCCTTCTGCCCTGCCGGGCCCGTCGGGAGGCGCCATG 337
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RESULT 14
US-11-060-756-2935
; Sequence 2935, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2935
; LENGTH: 1396
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-2935

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Query Match      56.9%;  Score 337;  DB 10;  Length 1396;
Best Local Similarity  100.0%;  Pred. No. 3.5e-83;
Matches  337;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    256 TGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGCCCGCTTTACTTGGTTGGGTTG 315
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGCCCGCTTTACTTGGTTGGGTTG 60

Qy    316 GGGGGGGCGGCGGGCGGGGCTGTTTTGTCCTTTGTCCTTTTCTTTTTCTTTTTTTAA 375
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGGGGGGCGGCGGGCGGGGCTGTTTTGTCCTTTGTCCTTTTCTTTTTCTTTTTTTAA 120

Qy    376 TTATCCAAACAGTGGGCAGCTTCCTCCCCACACCCAAGTATTGCACAATATTTGTGCG 435
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TTATCCAAACAGTGGGCAGCTTCCTCCCCACACCCAAGTATTGCACAATATTTGTGCG 180

Qy    436 GGGTATGGGGGTGGGTTTTAAATCTCGTTTCTTGGACAAGCACAGGGATCTCGTTCT 495
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GGGTATGGGGGTGGGTTTTAAATCTCGTTTCTTGGACAAGCACAGGGATCTCGTTCT 240

Qy    496 CCTCATTTTTGGGGGTGTGTGGGGACTTCTCAGTGTCGTGTCCCCAGCCTTCTCTCGCAGT 555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CCTCATTTTTGGGGGTGTGTGGGGACTTCTCAGTGTCGTGTCCCCAGCCTTCTCTCGCAGT 300

Qy    556 CCCTTCTGCCCTGCCGGGCCCGTCGGGAGGCGCCATG 592
          |||||||||||||||||||||||||||||||||||||
Db    301 CCCTTCTGCCCTGCCGGGCCCGTCGGGAGGCGCCATG 337
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RESULT 15
US-11-060-756-7207
; Sequence 7207, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin

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;   TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
;   TITLE OF INVENTION: Target Genes
;   FILE REFERENCE: AM101083 (031896-042000)
;   CURRENT APPLICATION NUMBER: US/11/060,756
;   CURRENT FILING DATE: 2005-02-18
;   NUMBER OF SEQ ID NOS: 303284
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7207
;   LENGTH: 1396
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-060-756-7207
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Query Match      56.9%;   Score 337;  DB 10;   Length 1396;
Best Local Similarity  100.0%;   Pred. No. 3.5e-83;
Matches  337;  Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

Qy     256  TGACTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTGCCCGCTTACTTTGGTTGGGTTG  315
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1  TGACTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTGCCCGCTTACTTTGGTTGGGTTG   60

Qy     316  GGGGGGGGCGGCGCGGGCTGTTTTGTTCCTTTCTTTTTTAAGAGTTGGGTTTCTTTTTTAA  375
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  GGGGGGGGCGGCGCGGGCTGTTTTGTTCCTTTCTTTTTTAAGAGTTGGGTTTCTTTTTTAA  120

Qy     376  TTATCCAAACAGTGGGCAGCTTCCTCCCCCACACCCAAGTATTTGCACAATATTTGTGCG  435
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121  TTATCCAAACAGTGGGCAGCTTCCTCCCCCACACCCAAGTATTTGCACAATATTTGTGCG  180

Qy     436  GGGTATGGGGGTGGGTTTTAAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCT  495
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181  GGGTATGGGGGTGGGTTTTAAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTTCT  240

Qy     496  CCTCATTTTTGGGGGTGTGTGGGGACTTCTCAGGTCGTGTCCCAGCCTTCTCTCTGCAGT  555
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241  CCTCATTTTTGGGGGTGTGTGGGGACTTCTCAGGTCGTGTCCCAGCCTTCTCTCTGCAGT  300

Qy     556  CCCTTCTGCCCTGCCGGGCCCGTCGGGAGGCGCCATG  592
            |||||||||||||||||||||||||||||||||||||
Db     301  CCCTTCTGCCCTGCCGGGCCCGTCGGGAGGCGCCATG  337
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Search completed: April 3, 2006, 05:55:10
Job time : 738 secs

GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2006, 05:40:07 ; Search time 1439 Seconds
(without alignments)
1642.707 Million cell updates/sec

Title: US-10-624-670-1
Perfect score: 592
Sequence: 1 ctatagggcacgcgtggtcg.........gcccgtcgggaggcgccatg 592

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA_New:*
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9: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq2:*
10: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq3:*
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12: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
13: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
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15: /SIDS5/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	46.6	7.9	5562	8	US-10-240-708-63	Sequence 63, Appl
	2	45.6	7.7	6156	8	US-10-240-708-60	Sequence 60, Appl
	3	45.2	7.6	22118	14	US-11-082-154A-18	Sequence 18, Appl
	4	43	7.3	995	10	US-10-301-480-611851	Sequence 611851,
	5	43	7.3	995	10	US-10-301-480-1225260	Sequence 1225260,
c	6	43	7.3	137454	9	US-10-330-773-365	Sequence 365, App
	7	42.6	7.2	7001	14	US-11-011-332A-103	Sequence 103, App
	8	42.6	7.2	8252	14	US-11-011-332A-158	Sequence 158, App
	9	42.4	7.2	8467	14	US-11-011-332A-96	Sequence 96, Appl
	10	42.2	7.1	3641	14	US-11-102-026A-181	Sequence 181, App
c	11	42	7.1	4453	14	US-11-011-332A-98	Sequence 98, Appl
c	12	41.6	7.0	587	6	US-09-925-065A-760778	Sequence 760778,
c	13	41.6	7.0	587	6	US-09-925-065A-760779	Sequence 760779,
c	14	41.6	7.0	59002	9	US-10-330-773-966	Sequence 966, App
c	15	41.4	7.0	614	6	US-09-925-065A-36845	Sequence 36845, A
c	16	41.4	7.0	614	9	US-10-301-480-138083	Sequence 138083,
c	17	41.4	7.0	614	10	US-10-301-480-751492	Sequence 751492,
c	18	41.4	7.0	28536	14	US-11-011-332A-156	Sequence 156, App
	19	41.2	7.0	19233	8	US-10-240-708-45	Sequence 45, Appl
	20	41	6.9	6499	14	US-11-011-332A-91	Sequence 91, Appl
c	21	40.8	6.9	635	8	US-10-920-625-60	Sequence 60, Appl
	22	40.8	6.9	5455	8	US-10-240-708-34	Sequence 34, Appl
	23	40.8	6.9	10490	14	US-11-011-332A-101	Sequence 101, App
	24	40.4	6.8	210920	9	US-10-330-773-99	Sequence 99, Appl
c	25	40.2	6.8	614	6	US-09-925-065A-36846	Sequence 36846, A
c	26	40.2	6.8	614	6	US-09-925-065A-36847	Sequence 36847, A
c	27	40.2	6.8	614	9	US-10-301-480-138084	Sequence 138084,
c	28	40.2	6.8	614	9	US-10-301-480-138085	Sequence 138085,
c	29	40.2	6.8	614	10	US-10-301-480-751493	Sequence 751493,
c	30	40.2	6.8	614	10	US-10-301-480-751494	Sequence 751494,
	31	40.2	6.8	666	6	US-09-925-065A-534678	Sequence 534678,
	32	40.2	6.8	892	10	US-10-301-480-539021	Sequence 539021,
	33	40.2	6.8	892	10	US-10-301-480-1152430	Sequence 1152430,
c	34	40	6.7	800	9	US-10-920-625-61	Sequence 61, Appl
	35	39.8	6.7	5666	8	US-10-240-708-29	Sequence 29, Appl
	36	39.6	6.7	6583	8	US-10-240-708-26	Sequence 26, Appl
	37	39.2	6.6	411	8	US-10-927-641-30	Sequence 30, Appl
	38	39.2	6.6	2791	11	US-11-192-123-1	Sequence 1, Appli
c	39	39.2	6.6	8467	14	US-11-011-332A-97	Sequence 97, Appl
	40	39.2	6.6	157224	14	US-11-112-908-51	Sequence 51, Appl
	41	39.2	6.6	170189	14	US-11-112-908-50	Sequence 50, Appl
c	42	39	6.6	810	11	US-11-096-568A-9782	Sequence 9782, Ap
c	43	39	6.6	1031	11	US-11-174-413-66	Sequence 66, Appl
	44	39	6.6	2240	11	US-11-166-234-6	Sequence 6, Appli
c	45	39	6.6	2344	9	US-10-920-625-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-10-240-708-63
; Sequence 63, Application US/10240708
; Publication No. US2005028257A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/240,708
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 63
; LENGTH: 5562
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-708-63

Query Match 7.9%; Score 46.6; DB 8; Length 5562;
Best Local Similarity 56.1%; Pred. No. 1.2;
Matches 88; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 217 GAGCTTTTTGGTTGTCTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAGA 276
            |||||| |||||||||||||||| ||||| ||||||||||||| |||
Db 3732 GATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAGGAAGTATTTAGTGTGGTAGG 3791

Qy 277 CGGGAGTTTGGAGTTGCCCGCTTACTTTGGTTGGTTGGGTTGGGGGGGGCGGCGGGGCTGTTT 336

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Db    3792  GTTTATTTGGAGTATTTAGTATGTTTAGTTGGTTTTGCGGGTGCGGGGTGTTTTGTT 3851
            |||           |  ||  |||||| || ||| ||||  |||| ||  |  |||||
Qy     337  GTTCCTTTCTTTTAAGAGTTGGTTTTCTTTTTT 373
            ||| | |||| ||||||
Db    3852  TTTTTTTTTTTTTTTTTTATGTGTTCGGTTTATATTTT 3888
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RESULT 2
US-10-240-708-60
; Sequence 60, Application US/10240708
; Publication No. US20050282157A1
; GENERAL INFORMATION:
;   APPLICANT: OLEK, Alexander
;   APPLICANT: PIEPENBROCK, Christian
;   APPLICANT: BERLIN, Kurt
;   TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
;   TITLE OF INVENTION: by Assessing DNA Methylation
;   FILE REFERENCE: 5013.1012
;   CURRENT APPLICATION NUMBER: US/10/240,708
;   CURRENT FILING DATE: 2002-10-03
;   PRIOR APPLICATION NUMBER: PCT/EP01/03971
;   PRIOR FILING DATE: 2001-04-06
;   PRIOR APPLICATION NUMBER: DE 10019058.8
;   PRIOR FILING DATE: 2000-04-06
;   PRIOR APPLICATION NUMBER: DE 10019173.8
;   PRIOR FILING DATE: 2000-04-07
;   PRIOR APPLICATION NUMBER: DE 10032529.7
;   PRIOR FILING DATE: 2000-06-30
;   PRIOR APPLICATION NUMBER: DE 10043826.1
;   PRIOR FILING DATE: 2000-09-01
;   NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 60
;   LENGTH: 6156
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-708-60

Query Match   7.7%; Score 45.6; DB 8; Length 6156;
Best Local Similarity   52.7%; Pred. No. 2;
Matches   99; Conservative   0; Mismatches   89; Indels   0; Gaps   0;

Qy   192 TTTGAGTTTTTAAGTTTCTTTGCTGAGCTTTTTGGTTGTCTTTTATTTTTTGCCTC 251
            ||||||||||||||| |||| |||||| |||||| | ||| | |||||||||
Db   1453 TTTTATTTTTTATTTTTTTAGTTTTGTTTAGTTTTTCGTATTTTCGTTGTATTTTACGCGTC 1512

Qy   252 TTTATGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGCCCCGCTTTACTTGGTTGG 311
            ||| |||||| ||||| ||||||||||| ||||||
Db   1513 GGGTTTAGTTAGAGAGTGTATTGAGGAAGAGCGGAGATTTTTTTTTTTTTAGTAGGT 1572

Qy   312 GTTGGGGGGGGCGCGGGGCGTGTTTGTCCTTTTCTTTTTTAAGAGTTGGGTTTTCTTTT 371
            |||||||||| || ||| ||||| ||| |||||
Db   1573 TGTGTCGGGGAGGGCCGGGGTTTATCGTTCGTTTTCGTCGTCGTTTTTTTTTTCGTTTTTTTT 1632

Qy   372 TTAATTAT 379
            || ||||
Db   1633 TTTTTTTT 1640

RESULT 3.
US-11-082-154A-18
; Sequence 18, Application US/11082154A
; Publication No. US20060024820A1
; GENERAL INFORMATION:
;   APPLICANT: Perkins, Edward
;   APPLICANT: Perez, Carl
;   APPLICANT: Lindenbaum, Michael
;   APPLICANT: Greene, Amy
;   APPLICANT: Leung, Josephine
;   APPLICANT: Fleming, Elena
;   APPLICANT: Stewart, Sandra

;   APPLICANT: Shellard, Joan
;   TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
;   FILE REFERENCE: 17084-022003 (420C)
;   CURRENT APPLICATION NUMBER: US/11/082,154A
;   CURRENT FILING DATE: 2005-03-15
;   PRIOR APPLICATION NUMBER: 60/294,758
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: 60/366,891
;   PRIOR FILING DATE: 2002-03-21
;   PRIOR APPLICATION NUMBER: US 10/161,403
;   PRIOR FILING DATE: 2002-05-30
;   NUMBER OF SEQ ID NOS: 129
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 22118
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: GenBank X82564
;   DATABASE ENTRY DATE: 1996-04-09
US-11-082-154A-18

Query Match   7.6%; Score 45.2; DB 14; Length 22118;
Best Local Similarity   52.7%; Pred. No. 3.3;
Matches   98; Conservative   0; Mismatches   88; Indels   0; Gaps   0;

Qy   192 TTTGAGTTTTTAAGTTTCTTTGCTGAGCTTTTTGGTTGTCTTTTATTTTTTGCCTC 251
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Db   19801 TTTGTGTGTTTTGTTTTGTTTTGTTTTTGTTTTTGTTTTGTTTTTTTGTTTTTTGT 19860

Qy   252 TTTATGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGTGTTGTGTGTTG 311
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Db   19861 TTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGGTTGGGGTTGGGGTTGGGGTTGG 19920

Qy   312 GTTGGGGGGGCGGCGGGGCGTGTTTTGTCGTGTTTGTTGTTTGGTTTTCTTTT 371
            ||||| | |||
Db   19921 GTTGGGTTGGGTTGGGTTGGTGTGTGTTTGGTGTTTGGTTTGGTGTTTTGTTTTGTT 19980

Qy   372 TTAATT 377
            || ||
Db   19981 TTGTTT 19986

RESULT 4
US-10-301-480-611851
; Sequence 611851, Application US/10301480
; Publication No. US2006005754A1
; GENERAL INFORMATION:
;   APPLICANT: Wang, David G.
;   TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
;   TITLE OF INVENTION: in the Human Genome
;   FILE REFERENCE: 108827.137
;   CURRENT APPLICATION NUMBER: US/10/301,480
;   CURRENT FILING DATE: 2002-11-21
;   PRIOR APPLICATION NUMBER: US 10/215,598
;   PRIOR FILING DATE: 2002-08-09
;   PRIOR APPLICATION NUMBER: US 60/311,695
;   PRIOR FILING DATE: 2001-08-10
;   NUMBER OF SEQ ID NOS: 1226818
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 611851
;   LENGTH: 995
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-611851

Query Match   7.3%; Score 43; DB 10; Length 995;
Best Local Similarity   51.9%; Pred. No. 5.1;
Matches   97; Conservative   0; Mismatches   90; Indels   0; Gaps   0;

Qy   187 TTCACTTTGAGTTTTAAGTTTCTTTGCTGAGCTTTTTGGTTGTCTTTTATTTTT 246
            || ||||| |||| ||||
Db   430 TTCAAAATGACTAATTTGCATTCTGTCTTTTGCTTTTGTAAATGAAGTTTTTTTTT 489
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; TYPE: DNA
; ORGANISM: Mus musculus
US-10-330-773-365

Query Match   7.3%; Score 43; DB 9; Length 137454;
Best Local Similarity 51.3%; Pred. No. 15;
Matches 100; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

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Qy     61 TTCTTCCTCTGGCCCTTGGGGGCTTTGGGGCGCCACCTCTGAGTGAAGGGGGTGTCGCCC 120
          |||||     |||||||||   |||||||
Db 115071 TTCTCTGTATAGCCCTGGCTGTCCTGGAGCTCACTTTGTAGACCAGGCTGCCTCGAATC 115012

Qy    121 ATCCACCAATGTGAGAGAGGGCGCCCCCGTGTGGGGTCCAGCTCTGGACACTGCTTGGCG 180
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Db 115011 AGAAATCCACCTGCCTCTGCCTCCCGAGTGCTGGGATTAAAGGCATGGCGCCACCATGCCC 114952

Qy    181 GCCGGGTTCACTTGAGTTTTAAGTTTCTTCGTGCTGAGCTTTTTTGGTGTTCTTTTTA 240
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Db 114951 GGCTTCTTCTTCTCTTTCTTTTTTTTTTTTTTTTTTGGATATTTTTTCTTTTTCTTTTT 114892

Qy    241 TTTTTGCCTCTTTA 255
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Db 114891 AATTTATTTTTTTA 114877
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RESULT 7
US-11-011-332A-103
; Sequence 103, Application US/11011332A
; Publication No. US2006002464A1
; GENERAL INFORMATION:
;   APPLICANT: Foekens, John
;   APPLICANT: Harbeck, Nadia
;   APPLICANT: Koenig, Thomas
;   APPLICANT: Maier, Sabine
;   APPLICANT: Martens, John
;   APPLICANT: Model, Fabian
;   APPLICANT: Nimmrich, Inko
;   APPLICANT: Rujan, Tamas
;   APPLICANT: Schmitt, Manfred
;   APPLICANT: Leesche, Ralf
;   APPLICANT: Dietrich, Dimo
;   APPLICANT: Mueller, Volkmar
;   APPLICANT: Kluth, Antje
;   APPLICANT: Schwope, Ina
;   APPLICANT: Hartmann, Oliver
;   APPLICANT: Adorjan, Peter
;   TITLE OF INVENTION: PROGNOSTIC MARKERS FOR PREDICTION OF TREATMENT RESPONSE AND/OR S
;   TITLE OF INVENTION: BREAST CELL PROLIFERATIVE DISORDER PATIENTS
;   FILE REFERENCE: 47675-99
;   CURRENT APPLICATION NUMBER: US/11/011,332A
;   CURRENT FILING DATE: 2004-12-13
;   PRIOR APPLICATION NUMBER: US 10/517,741
;   PRIOR FILING DATE: 2003-10-01
;   PRIOR APPLICATION NUMBER: PCT/EP2003/010881
;   PRIOR FILING DATE: 2003-10-01
;   PRIOR APPLICATION NUMBER: DE 10245779.4
;   PRIOR FILING DATE: 2002-10-01
;   PRIOR APPLICATION NUMBER: DE 10300096.8
;   PRIOR FILING DATE: 2003-01-07
;   PRIOR APPLICATION NUMBER: DE 10317955.0
;   PRIOR FILING DATE: 2003-04-17
;   PRIOR APPLICATION NUMBER: PCT/EP2004/014170
;   PRIOR FILING DATE: 2004-12-13
;   PRIOR APPLICATION NUMBER: EP 03090432.0
;   PRIOR FILING DATE: 2003-12-11
;   PRIOR APPLICATION NUMBER: EP 04090041.7
;   PRIOR FILING DATE: 2004-02-10
;   PRIOR APPLICATION NUMBER: EP 04090380.9
;   PRIOR FILING DATE: 2004-09-30
;   PRIOR APPLICATION NUMBER: EP 04090127.4
;   PRIOR FILING DATE: 2004-04-01
;   Remaining Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 158

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Qy    247 GCCTCTTATGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGCCCGCTTTACTTTG 306
          |||||||
Db    490 TTTTTTTTTCTCCTTTAATGCATAGACACTGCAGTTTCCTTTAGTCAAATACAAGTTA 549

Qy    307 GTTGGGTTGGGGGGCGGCGGCCGTGTTTTGTTCCTTTTTTTTTAAGAGTTGGGTTTT 366
          ||||||    |||||   ||||||
Db    550 ATTGTGTGTGTGAGTGCGTGCACGGGTTCCTTTGTGCACGGGTTCCTTTGAAAGGATGGTTTG 609

Qy    367 CTTTTT 373
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Db    610 CTGATCT 616
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RESULT 5
US-10-301-480-1225260
; Sequence 1225260, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;   APPLICANT: Wang, David G.
;   TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
;   TITLE OF INVENTION: in the Human Genome
;   FILE REFERENCE: 108827.137
;   CURRENT APPLICATION NUMBER: US 10/301,480
;   CURRENT FILING DATE: 2002-11-21
;   PRIOR APPLICATION NUMBER: US 10/215,598
;   PRIOR FILING DATE: 2002-08-09
;   PRIOR APPLICATION NUMBER: US 60/311,695
;   PRIOR FILING DATE: 2001-08-10
;   NUMBER OF SEQ ID NOS: 1226818
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1225260
; LENGTH: 995
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1225260

Query Match   7.3%; Score 43; DB 10; Length 995;
Best Local Similarity 51.9%; Pred. No. 5.1;
Matches 97; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

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Qy    187 TTCACTTGAGTTTTAAGTTTCTTTGCTGAGCTTTTTTGGTTGTTCTTTTTTATTTTTT 246
          ||||||   |||||    ||||   ||||||   |||||||
Db    430 TTCAAAATGACTAATTTTTGCATTCTGGTCTTTGCTTTGTAAATGAAGTTTTTTTTTT 489

Qy    247 GCCTCTTATGACTATCCAGCTCTGAGAGACGGGAGTTGGAGTTGCCCGCTTTACTTTG 306
          |||||||
Db    490 TTTTTTTTTCTCCTTTAATGCATAGACACTGCAGTTTCCTTTAGTCAAATACAAGTTA 549

Qy    307 GTTGGGTTGGGGGGCGGCGGCCGTGTTTTGTTCCTTTTTTTTTAAGAGTTGGGTTTT 366
          ||||||    |||||   ||||||
Db    550 ATTGTGTGTGTGAGTGCGTGCACGGGTTCCTTTGTGCACGGGTTCCTTTGAAAGGATGGTTTG 609

Qy    367 CTTTTT 373
          ||| ||
Db    610 CTGATCT 616
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RESULT 6
US-10-330-773-365/c
; Sequence 365, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
;   APPLICANT: David W. Morris
;   APPLICANT: Marc Malandro
;   TITLE OF INVENTION: Novel Compositions and Methods in Cancer
;   FILE REFERENCE: 52945200130 0
;   CURRENT APPLICATION NUMBER: US/10/330,773
;   CURRENT FILING DATE: 2002-12-27
;   NUMBER OF SEQ ID NOS: 981
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 365
; LENGTH: 137454

; SEQ ID NO 103
; LENGTH: 7001
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-11-011-332A-103

Query Match   7.2%; Score 42.6; DB 14; Length 7001;
Best Local Similarity 52.5%; Pred. No. 9.7;
Matches 93; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy   199 TTTTAAGTTTCTTTGCTGAGCTTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATGA 258
         |||||||||||||| ||||||||| |||||| |||| ||||
Db 6296 TTTTGGGTATTTTGGGATGATGGTTTTGGTGTGTTGTGTTTTTGTTTTTTTT 6355

Qy   259 CTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTGCCCGCTTTACTTTGGTTGGGTTGGGG 318
         ||||||||||| ||| |||||||| ||||||||||||||
Db 6356 TTATTAGATTTTTAGATTTTTTTTTTTTTTTGAGATGGAGTTTGTTTTGTTTGTTATTT 6415

Qy   319 GGGGGCGGCGGGCGTGTTTTGTTGTCCTTTTGTTCCTTTTCTTTTTTAA 375
         ||| ||| |||| ||||| |||||
Db 6416 AGGTTGGAGTGTAATGGTGTGATTTTGGTTTATTATAATTTTGTTTTTTTGGGTTTA 6472

RESULT 8
US-11-011-332A-158
; Sequence 158, Application US/11011332A
; Publication No. US20060024684A1
; GENERAL INFORMATION:
;   APPLICANT: Foekens, John
;   APPLICANT: Harbeck, Nadia
;   APPLICANT: Koenig, Thomas
;   APPLICANT: Maier, Sabine
;   APPLICANT: Martens, John
;   APPLICANT: Model, Fabian
;   APPLICANT: Nimmrich, Inko
;   APPLICANT: Rujan, Tamas
;   APPLICANT: Schmitt, Manfred
;   APPLICANT: Leesche, Ralf
;   APPLICANT: Dietrich, Dimo
;   APPLICANT: Mueller, Volkmar
;   APPLICANT: Kluth, Antje
;   APPLICANT: Schwope, Ina
;   APPLICANT: Hartmann, Oliver
;   APPLICANT: Adorjan, Peter
;   TITLE OF INVENTION: PROGNOSTIC MARKERS FOR PREDICTION OF TREATMENT RESPONSE AND/OR SU
;   TITLE OF INVENTION: BREAST CELL PROLIFERATIVE DISORDER PATIENTS
;   FILE REFERENCE: 47675-99
;   CURRENT APPLICATION NUMBER: US/11/011,332A
;   CURRENT FILING DATE: 2004-12-13
;   PRIOR APPLICATION NUMBER: US 10/517,741
;   PRIOR FILING DATE: 2003-10-01
;   PRIOR APPLICATION NUMBER: PCT/EP2003/010881
;   PRIOR FILING DATE: 2003-10-01
;   PRIOR APPLICATION NUMBER: DE 10245779.4
;   PRIOR FILING DATE: 2002-10-01
;   PRIOR APPLICATION NUMBER: DE 10300096.8
;   PRIOR FILING DATE: 2003-01-07
;   PRIOR APPLICATION NUMBER: DE 10317955.0
;   PRIOR FILING DATE: 2003-04-17
;   PRIOR APPLICATION NUMBER: PCT/EP2004/014170
;   PRIOR FILING DATE: 2004-12-13
;   PRIOR APPLICATION NUMBER: EP 03090432.0
;   PRIOR FILING DATE: 2003-12-11
;   PRIOR APPLICATION NUMBER: EP 04090041.7
;   PRIOR FILING DATE: 2004-02-10
;   PRIOR APPLICATION NUMBER: EP 04090380.9
;   PRIOR FILING DATE: 2004-09-30
;   PRIOR APPLICATION NUMBER: EP 04090127.4
;   PRIOR FILING DATE: 2004-04-01
;   Remaining Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 158

; SEQ ID NO 158
; LENGTH: 8252
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-11-011-332A-158

Query Match   7.2%; Score 42.6; DB 14; Length 8252;
Best Local Similarity 52.5%; Pred. No. 10;
Matches 93; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy   199 TTTTAAGTTTCTTTGCTGAGCTTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATGA 258
         |||||||||||||| ||||||||| |||||| |||| ||||
Db 4335 TTTTGGGTATTTTGGGATGATGGTTTTGGTGTGTTGTGTTTTTGTTTTTTTT 4394

Qy   259 CTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTGCCCGCTTTACTTTGGTTGGGTTGGGG 318
         ||||||||||| ||| |||||||| ||||||||||||||
Db 4395 TTATTAGATTTTTAGATTTTTTTTTTTTTTTGAGATGGAGTTTGTTTTGTTTGTTATTT 4454

Qy   319 GGGGGCGGCGGGCGTGTTTTGTTGTCCTTTTGTTCCTTTTCTTTTTTAA 375
         ||| ||| |||| ||||| |||||
Db 4455 AGGTTGGAGTGTAATGGTGTGATTTTGGTTTATTATAATTTTGTTTTTTTGGGTTTA 4511

RESULT 9
US-11-011-332A-96
; Sequence 96, Application US/11011332A
; Publication No. US20060024684A1
; GENERAL INFORMATION:
;   APPLICANT: Foekens, John
;   APPLICANT: Harbeck, Nadia
;   APPLICANT: Koenig, Thomas
;   APPLICANT: Maier, Sabine
;   APPLICANT: Martens, John
;   APPLICANT: Model, Fabian
;   APPLICANT: Nimmrich, Inko
;   APPLICANT: Rujan, Tamas
;   APPLICANT: Schmitt, Manfred
;   APPLICANT: Leesche, Ralf
;   APPLICANT: Dietrich, Dimo
;   APPLICANT: Mueller, Volkmar
;   APPLICANT: Kluth, Antje
;   APPLICANT: Schwope, Ina
;   APPLICANT: Hartmann, Oliver
;   APPLICANT: Adorjan, Peter
;   TITLE OF INVENTION: PROGNOSTIC MARKERS FOR PREDICTION OF TREATMENT RESPONSE AND/OR SI
;   TITLE OF INVENTION: BREAST CELL PROLIFERATIVE DISORDER PATIENTS
;   FILE REFERENCE: 47675-99
;   CURRENT APPLICATION NUMBER: US/11/011,332A
;   CURRENT FILING DATE: 2004-12-13
;   PRIOR APPLICATION NUMBER: US 10/517,741
;   PRIOR FILING DATE: 2003-10-01
;   PRIOR APPLICATION NUMBER: PCT/EP2003/010881
;   PRIOR FILING DATE: 2003-10-01
;   PRIOR APPLICATION NUMBER: DE 10245779.4
;   PRIOR FILING DATE: 2002-10-01
;   PRIOR APPLICATION NUMBER: DE 10300096.8
;   PRIOR FILING DATE: 2003-01-07
;   PRIOR APPLICATION NUMBER: DE 10317955.0
;   PRIOR FILING DATE: 2003-04-17
;   PRIOR APPLICATION NUMBER: PCT/EP2004/014170
;   PRIOR FILING DATE: 2004-12-13
;   PRIOR APPLICATION NUMBER: EP 03090432.0
;   PRIOR FILING DATE: 2003-12-11
;   PRIOR APPLICATION NUMBER: EP 04090041.7
;   PRIOR FILING DATE: 2004-02-10
;   PRIOR APPLICATION NUMBER: EP 04090380.9
;   PRIOR FILING DATE: 2004-09-30
;   PRIOR APPLICATION NUMBER: EP 04090127.4
;   PRIOR FILING DATE: 2004-04-01
;   Remaining Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 158

; SEQ ID NO 96
; LENGTH: 8467
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-11-011-332A-96

Query Match 7.2%; Score 42.4; DB 14; Length 8467;
Best Local Similarity 49.5%; Pred. No. 11;
Matches 109; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

```
Qy   160  AGCTCTGGACACTGCTTGGCGCGCCGGTCACTTGAGTTTTAAGTTTCTTGCTGAG  219
               ||| ||    ||||| |   || ||||||||  | ||||||  |||||||||
Db  4641  AGTTTTGTATAGTTGTTGTTTTGGAGTTGTGAGTTTAGGTTTTATTTTGATTTTTTGGG  4700

Qy   220  CTTTTTGGTTGTTCTTTTATTTTGCCTCTTTATGACTATCCAGCTCTGAGAGACGG  279
               ||||||  |||||||||||||      || ||||| |  |||||||||||||||
Db  4701  TTTTTTTTGTATTGTTGAGTTTAGTTTGTGGGGTGTATTAATGTTTGATAGGGTT  4760

Qy   280  GAGTTTGGAGTTGCCCCGCCTTACTTGGTTGGTTGGGGGGGCGGCCTGTTTTGTT  339
               | |||| ||||     ||| || ||||||  | |||||||||||||| |||||
Db  4761  GGGGAATGTGATAGGTAGTAGGTTTTATTTGGGTTTGGGGGAGGGGAGTTTTTTGTTTTTGAT  4820

Qy   340  CCTTTCTTTTTAAGAGTTGGGGTTTTTCTTTTTAATTAT  379
               ||||| ||||| |||||||||| ||||||||
Db  4821  AGTATTTTTTTTGTTTGTTGGTGGTGGATTTTTATTTTT  4860
```

RESULT 10
US-11-102-026A-181
; Sequence 181, Application US/11102026A
; Publication No. US2006021087A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; APPLICANT: Baum, James A
; APPLICANT: Gilbertson, Larry A
; APPLICANT: Kovalic, David K
; APPLICANT: LaRosa, Thomas J
; APPLICANT: Lu, Maolong
; APPLICANT: Munyikwa, Tichifa R. I.
; APPLICANT: Roberts, James K
; APPLICANT: Wu, Wei
; APPLICANT: Zhang, Bei
; TITLE OF INVENTION: Compositions and Methods for Control of Insect Infestations in Pl
; FILE REFERENCE: 38-21(53596)
; CURRENT APPLICATION NUMBER: US/11/102,026A
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60560842
; PRIOR FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60565632
; PRIOR FILING DATE: 2004-04-27
; PRIOR APPLICATION NUMBER: 60579062
; PRIOR FILING DATE: 2004-06-11
; PRIOR APPLICATION NUMBER: 60603421
; PRIOR FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: 60617261
; PRIOR FILING DATE: 2004-10-11
; PRIOR APPLICATION NUMBER: 60669241
; PRIOR FILING DATE: 2005-04-07
; NUMBER OF SEQ ID NOS: 190
; SEQ ID NO 181
; LENGTH: 3641
; TYPE: DNA
; ORGANISM: Lygus hesperus
US-11-102-026A-181

Query Match 7.1%; Score 42.2; DB 14; Length 3641;
Best Local Similarity 48.2%; Pred. No.10;
Matches 119; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

```
Qy   182  CCGGGGTCACTTGAGTTTTAAGTTTCTTTGCTGAGCTTTTTGGTTGTTCTTTTTAT  241
               ||  ||     | |||||  |||| |||| |   ||| || | |||| | |||||
```

Db   769 CCCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 828
```
               || ||| |
```
Qy   242 TTTTTGCCTCTTTATGACTATCCAGCTCTGAGAGACGGAGTTGGAGTTGCCCGCCTTTA 301
```
               |||||                                              |||
```
Db   829 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 888
```

Qy   302  CTTTGGTTGGTTGGGGGGGCGGCCGGCGGAGTTTTCCTTTCTTTTGTTCCTTTTTT  361
```
               ||| ||||| |||| ||||| ||| |||||
```
Db   889  TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT  948
```

Qy   362 GTTTTCTTTTTATTATTCCAAACAGTGGCAGCAGTTCCTCCCCACCACCCAAGTATTGC 421
```
               ||||||||||
```
Db   949 TTTTTTTTTTTTTTTCGGTAGTAAATGTTGAGTGTAATCTCAAACAACATATAAATAT 1008

Qy   422 ACAATAT 428
               ||||||
Db 1009 ATAAAAT 1015

RESULT 11
US-11-011-332A-98
; Sequence 98, Application US/11011332A
; Publication No. US20060024684A1
; GENERAL INFORMATION:
; APPLICANT: Foekens, John
; APPLICANT: Harbeck, Nadia
; APPLICANT: Koenig, Thomas
; APPLICANT: Maier, Sabine
; APPLICANT: Martens, John
; APPLICANT: Model, Fabian
; APPLICANT: Nimmrich, Inko
; APPLICANT: Rujan, Tamas
; APPLICANT: Schmitt, Manfred
; APPLICANT: Lesche, Ralf
; APPLICANT: Dietrich, Dimo
; APPLICANT: Mueller, Volkmar
; APPLICANT: Kluth, Antje
; APPLICANT: Schwope, Ina
; APPLICANT: Hartmann, Oliver
; APPLICANT: Adorjan, Peter
; TITLE OF INVENTION: PROGNOSTIC MARKERS FOR PREDICTION OF TREATMENT RESPONSE AND/OR S
; TITLE OF INVENTION: BREAST CELL PROLIFERATIVE DISORDER PATIENTS
; FILE REFERENCE: 47675-99
; CURRENT APPLICATION NUMBER: US/11/011,332A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US 10/517,741
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: PCT/EP2004/014170
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: EP 03090432.0
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: EP 04090041.7
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: EP 04090380.9
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: EP 04090127.4
; PRIOR FILING DATE: 2004-04-01
; Remaining Prior Application data removed -. See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 98
; LENGTH: 4453
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

US-11-011-332A-98

Query Match   7.1%;   Score 42;   DB 14;   Length 4453;
Best Local Similarity   49.5%;   Pred. No. 12;
Matches   108;   Conservative   0;   Mismatches   110;   Indels   0;   Gaps   0;

Qy   160   AGCTCTGGACACTGCTTGGCGCGCCGGGTTCACTTGAGTTTTAAGTTTTCTTTGCTGAG   219
              || || | || | ||| |||| |||||| ||
Db   2010   AGTTGGGGAGTTGGTTATTGTGGGTATTTTTTTTGTTGTTAGTAGTTGTTGTTTGGGTTTG   2069

Qy   220   CTTTTTGGTTGTTCTTTTTATTTTTGCCTCTTTATGACTATCCAGCTCTGAGAGACGG   279
              |||||| || | ||| || ||||
Db   2070   TTTTTTTGTTTTTGTTTTTTTGTTTTGATTTTTTTTTTTTTGTTAGAGTTGTTGTTTAG   2129

Qy   280   GAGTTTGGAGTTGCCCGCTTACTTGGTTGGGTTGGGTTGGGGGGGGGGCGGGCTGTTTTGTT   339
              |||| ||| || ||||| | |||| ||||
Db   2130   TGTTTTTGATTTTGTTATTATGAGAGTTTTGTTGGTGTGTGTTGTTTTTGTGTTTTGGTT   2189

Qy   340   CCTTTTCTTTTTTAAGAGTTGGGTTTTCTTTTTTAATT   377
              | |||| ||| ||| |||
Db   2190   GTGAGTGATTTTAAAGTGAGTGTGTGTTGTTTTGATT   2227

RESULT 12
US-09-925-065A-760778/c
; Sequence 760778, Application US/09925065A
; Publication No. US2004018104BA1
; GENERAL INFORMATION:
;   APPLICANT: Wang, David G.
;   TITLE OF INVENTION: Identification and Mapping of Single
;   TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
;   FILE REFERENCE: 108827.135
;   CURRENT APPLICATION NUMBER: US/09/925,065A
;   CURRENT FILING DATE: 2001-08-08
;   PRIOR APPLICATION NUMBER: US 60/243,096
;   PRIOR FILING DATE: 2000-10-24
;   PRIOR APPLICATION NUMBER: US 60/252,147
;   PRIOR FILING DATE: 2000-11-20
;   PRIOR APPLICATION NUMBER: US 60/250,092
;   PRIOR FILING DATE: 2000-11-30
;   PRIOR APPLICATION NUMBER: US 60/261,766
;   PRIOR FILING DATE: 2001-01-16
;   PRIOR APPLICATION NUMBER: US 60/289,846
;   PRIOR FILING DATE: 2001-05-09
;   NUMBER OF SEQ ID NOS: 957086
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 760778
;   LENGTH: 587
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-760778

Query Match   7.0%;   Score 41.6;   DB 6;   Length 587;
Best Local Similarity   53.0%;   Pred. No. 9.3;
Matches   89;   Conservative   0;   Mismatches   79;   Indels   0;   Gaps   0;

Qy   198   TTTTTAAGTTTCTTCTTGCTGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATG   257
              |||| |||||| || ||||| | | ||| || | || || | ||||
Db   171   TCTTCTATTTTTTTCTTCATTAGTATGGTAGAAGTTCTGTCAATTCTGTTTATCTTCTCA   112

Qy   258   ACTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTGCCCGCTTACTTGGTTGGGTTGGG   317
              | | || | || |||| | |||| ||| ||
Db   111   AAAACCCAACTTTGTTCCTTGATTTTGTATTGTTTTCTTAACTTCAAATTCATTTAT   52

Qy   318   GGGGGCGGCGGGCTGTTTTGTTCCTTTTCTTTTTTTAAGAGTTGGGTT   365
              |||||||||||||| |||||| ||| |||| |
Db   51   TTCTGCTCTGGTCTTTTATTATTTCTTTTTCTTTCTATTAAATTTGGGTTT   4

RESULT 13
US-09-925-065A-760779/c
; Sequence 760779, Application US/09925065A
; Publication No. US2004018104BA1

───

Query Match   7.0%;   Score 41.6;   DB 6;   Length 587;
Best Local Similarity   53.0%;   Pred. No. 9.3;
Matches   89;   Conservative   0;   Mismatches   79;   Indels   0;   Gaps   0;

Qy   198   TTTTTAAGTTTCTTCTTGCTGAGCTTTTTGGTTGTTCTTTTATTTTTGCCTCTTTATG   257
              |||| |||||| || ||||| | | ||| || | || || | ||||
Db   171   TCTTCTATTTTTTTCTTCATTAGTATGGTAGAAGTTCTGTCAATTCTGTTTATCTTCTCA   112

Qy   258   ACTATCCAGCTCTGAGAGACGGGAGTTTGGAGTTGCCCGCTTACTTGGTTGGGTTGGG   317
              | | || | || |||| | |||| ||| ||
Db   111   AAAACCCAACTTTGTTCCTTGATTTTGTATTGTTTTCTTAACTTCAAATTCATTTAT   52

Qy   318   GGGGGCGGCGGGCTGTTTTGTTCCTTTTCTTTTTTTTAAGAGTTGGGTT   365
              |||||||||||||| |||||| ||| |||| |
Db   51   TTCTGCTCTGGTCTTTTATTATTTCTTTTTCTTTCTATTAAATTTGGGTTT   4

RESULT 14
US-10-330-773-966/c
; Sequence 966, Application US/10330773
; Publication No. US2006004026A1
; GENERAL INFORMATION:
;   APPLICANT: David W. Morris
;   APPLICANT: Marc Malandro
;   TITLE OF INVENTION: Novel Compositions and Methods in Cancer
;   FILE REFERENCE: 52945200l300
;   CURRENT APPLICATION NUMBER: US/10/330,773
;   CURRENT FILING DATE: 2002-12-27
;   NUMBER OF SEQ ID NOS: 981
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 966
;   LENGTH: 59002
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(59002)
;   OTHER INFORMATION: n = A,T,C or G
US-10-330-773-966

Query Match   7.0%;   Score 41.6;   DB 9;   Length 59002;
Best Local Similarity   54.6%;   Pred. No. 26;
Matches   83;   Conservative   0;   Mismatches   69;   Indels   0;   Gaps   0;

Qy   221   TTTTTTGGTTGTTCTTTTTATTTTTGCCTCTTCTTTATGACTATCCAGCTCTGAGAGACGGG   280
              ||||||| |||||| |||| | || ||| ||||| ||||| || ||||| |||||
Db   9617   TTTTTTGTTGTGTTGGTTGTTGGTTGGTTGGTTGGTTTTGGTTTGGTTTTGGTT   9558

```
Qy    281 AGTTTGGAGTTGCCCGCTTTACTTGGTTGGGTTGGGGGGGGCGGCGGCTGTGTTTGTTC 340
          |||||| ||| ||||||||||||||||||||||||||        ||  |||||||||
Db   9557 GGTTTGGTTTGGTTTGGTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTT 9498

Qy    341 CTTTTCTTTTTAAGAGTTGGGTTTCTTTT 372
          |||      ||| ||||| |||| |||||
Db   9497 GGTTTGGTTTGGTTTGGTTTGGTTTGGTTT 9466
```

RESULT 15
US-09-925-065A-36845/c
; Sequence 36845, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36845
; LENGTH: 614
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-36845

Query Match   7.0%; Score 41.4; DB 6; Length 614;
Best Local Similarity   53.5%; Pred. No. 10;
Matches   84; Conservative   1; Mismatches   72; Indels   0; Gaps   0;

Qy   197 GTTTTTAAGTTTCTTTGCTGAGCTTTTTGGTTGTTCTTTTTATTTTTTGCCTCTTTAT 256
          ||||||||||||||||||||| ||||||||||:||||| ||||||| |||||||
Db   364 GTTCTTTCTTTTCTTTTTCCTTTCCTTCTTTTCTTTTTTTTTTTTTYTTTTTTTGAGACC 305

Qy   257 GACTATCCAGCTCTGAGAGACCGGGAGTTTGGAGTTGCCCGCTTTACTTGGTTGGGTTGG 316
          || ||| | | ||| ||||| ||| |||| || | || | |
Db   304 GAGTCTTGCTCTGTCACCCAGGCTGAAGTGCAGTGGTGCAATCCTCGCTCGCTGCAAAGT 245

Qy   317 GGGGGCCGCGGCGGCTGTTTGTTCCTTTTCTTTTTTA 353
          || | | | ||||||||||||
Db   244 TTGGAGGTTCTTTTTTTTTTTTTTTTCTTTTCTTTTGA 208
```

Search completed: April  3, 2006, 07:02:20
Job time : 1441 secs